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Human ORFX ORF3125	Arabidopsis thalia	Human oxidoreducta	Amino acid sequenc	Short-chain dehydr	21615 ADH. HOMO S	Human Flo peptide	Actinomadura hibis	Human secreted pro	Human gastric canc	Arabidopsis thalia	Drosophila melanog	Putative P. abyssi	Streptococcus poly	Lactobacillus keti	Collamydia pneumoni	Ditative D abyesi	Recombinant mosqui	Aed a 3 cDNA clone	Arabidopsis thalia	Arabidopsis thalia	Drosophila melanog	Salmonella tymbi c	Propionibacterium	Arabidopsis transc	Drosophila melanog	C. glutamicum SRT	Streptococcus poly	Arabidopsis thalia	Drosophila melahog	Human liver peptid	Drosophila melanog	Drosophila melanog	Klebsiella pneumon	Propionipacterium Dentide #4420 enco	Peptide #4501 enco	Protein #4309 enco	Human brain expres	Peptide #4403 enco	Peptide #4510 enco	Peptide #4286 enco	Arabidopsis thalia	Alzheimer-associat	Human short chain	prehidonsis thalia	Drosophila melanog	Escherichia coli p	Streptococcus poly	Human nucleic acid	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Human protein clon	Human secreted pro	hur	H. pylori ORF hp4p	Drosophila melanod	Propionibacterium	Staphylococcus epi
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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the ligana biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular care weight of 27-31 KDa, an isoalactric point of 5.9-6.85, and require weight of 27-31 KDa, an isoalactric point of 5.9-6.85, and require comparing the national care acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan of secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairssinol. The secoisolariciresinol dehydrogenase of proteins and mucleic acids can be utilized to: elevate or otherwise care the enzymes of health-protecting lignans, including phytoseprotect and mucleic acids can be utilized to: elevate or otherwise cause mucleic acids can be utilized to: elevate or otherwise vegetables, grains and fruits and to food items incorporating material vegetables, grains and fruits and to food items incorporating material vegetables, provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriceuticals and dietary cause properties, to genetically alter living organisms to produce an example (-)-tradeposenticals and (-)-tradepo

New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans

Claim 8; Page 46-47; 66pp; English.

Lewis NG;

Davin LB,

Costa MA,

WPI; 2000-126356/11. N-PSDB; AAZ45730.

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Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan, matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-bodophyllotoxin.
                                                                            Secoisolariciresinol dehydrogenase protein clone DEHY133.
            AAY54412 standard; Protein; 273 AA
                                                      (first entry)
                                                                                                                                                      Forsythia intermedia.
                                                                                                                                                                          WO9955846-Al
                                                      06-APR-2000
                                  AAY54412;
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99WO-US08975 98US-0082977

23-APR-1999;

Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan, matairesinol; health-protecting lignan; phytocetrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; Secoisolariciresinol dehydrogenase protein clone DEHY130. AAY54420 standard; Protein; 272 AA (first entry) 06-APR-2000 g g ò

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61 NSTYIHCDVINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSV 120

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1 MOLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS

100.0%; Score 273; DB 21; Length 273; 100.0%; Pred. No. 1.5e-270; tive 0; Mismatches 0; Indels 0

Query Match Best Local Similarity 100. Matches 273; Conservative

Sequence 273 AA;

61 NSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSV

121 NVTGVFLCMKHAARVMIPARSGNIISTASLSSTWGGGSSHAYCGSKHAVLALTRNLÄVEL

181 GOFGIRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLA

121 NVTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVEL

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(-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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100.0%; Pred. No. 1.6e-269;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                              Example 2; Page 61-63; 66pp; English
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properties, and (-)-podophyllotoxin.
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Matches 272; Conservative
                                    Forsythia intermedia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kba, an isolectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
                                                                                                                                                                                                                                                                                                          Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                          lignan; matairesinol; health protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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                                                                                                                                                                                                                             Secoisolariciresinol dehydrogenase protein clone SMDEHY321.
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AAY54413 standard; Protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Costa MA, Davin LB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Forsythia intermedia.
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Matches 110; Conserv
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                                                                                                                                                 06-APR-2000
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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.96.85, and require hot or NAPP as a coffactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of the enzymes. It is also used to obtain expression or enhanced expression of biosyntheeis. The enzyme is used for production of the pharmacologically active lignan, matairesinol The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise such as enterolactone and enterodiol, in plant species, including phycostical enterolactors and enterodiol, in plant species, including material derived from such genetically altered plants; supplements; to genetically alter living organisms to produce an abundant, natural supply of lighans useful for supplements; to genetically pure lighans having desirable biological properties, for example (-)-traceledgemin which possesses antiviral properties, and (-)-podophyllotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
                                                                                                                                                                                                Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan; matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodactone; enterodactone; controcentical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophylocoxin.
                                                                                                                                                         Secoisolariciresinol dehydrogenase protein clone SMDEHY431.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis NG;
                                                                                                                                                                                                                                                                                                                                                                                 'note= "encoded by GTN"
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                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                       AAY54414 standard; Protein; 273 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0082977
                                                                                                                     (first entry)
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N-PSDB; AAZ45732.
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                                                                              AAY54414;
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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway.

The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require the secoisolariciresinol dehydrogenase proteins and engine of 27-31 kDa, an isoelectric point of 5.9-6.85, and require to mode of the secoisolariciresinol dehydrogenase in the salso used to obtain expression or enhanced expression of the enzymes. The enzyme is used for production of the pharmacologically active lignan, matairesinol and production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise context and enclar of health-protecting lignans, including phytosetrogenes and nucleic acids can be utilized to: elevate or otherwise such as enterolactone and entercadiol, in plant species, including phytosetric derived from such genetically allered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriculals and dietary supplements; to genetically alter living organisms to produce an abundant, purchasely experience, for example as neutriculals and dietary supplements; to genetically pure lignans having desirable biological properties, for example (-)-transferongenium which possesses antiviral process.
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                                                                                                                                                                                                                                                                                  Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan, matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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                                                                                                                                                                                                                                              Secoisolariciresinol dehydrogenase protein clone SMDEHY631.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SNSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMF
SNSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMF
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                                                                                                                        AAY54416 standard; Protein; 276 AA
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Best Local Similarity 100.0
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            Forsythia intermedia.
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N-PSDB; AAZ45734.
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Gaps

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Query Match
12.5%; Score 34; DB 21; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.2e-26;
Matches 34; Conservative 0; Mismatches 0; Indels

60 SNSTYIHCDVINEDGVKNAVDNTVSTYGKLDIMF 93

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AA021494

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recoisolaricires. Outside the properties of the pharmacologically biosynthesis. The enzyme is used for production of the pharmacologically biosynthesis. The enzyme is used for production of the pharmacologically active lighan, matairesinol. The secoisolariciresinol dehydrogenase proteins and nucleic acids can be utilized to: elevate or otherwise alter the levels of health-protecting lignans, including phycoestrogens such as enterolactone and enterodiol, in plant species, including vegetables, grains and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kba, an isoelectric point of 5.9-6.85, and require NAD or NADP as a coffactor. The secoisolariciresinol dehydrogenase nucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
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Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;
                     lignan; matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 277;
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hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 TAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNS
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ive 0; Mismatches
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properties, and (-)-podophyllotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                           Costa MA, Davin LB,
                                                                                                                                                                                                                                                       99WO-US08975.
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                                                                                                              Forsythia intermedia
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-126356/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAZ45733.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           content in seeds of a monocotyledon plant, comprising selecting at least formation, stably transforming a monocotyledon plant with chimeric gene (CG) constructs having a seed-specific transcriptional regulatory region operably linked to a nucleic acid sequence encoding the enzyme. The method of the invention is useful for stably transforming a monocotyledonous plant (e.g. rice) with CG constructs resulting in increased expression of the genes encoded by CG constructs. The G-lignan enriched seed composition is useful as a food additive. This sequence represents the secoisolariciresinol dehydrogenase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a method for increasing the guaiacyl (G)-lignan
                                                                                                                                                                                                                                                Guaiacyl (G)-lignan, monocotyledon plant, rice, food additive,
seed-specific transcriptional regulatory region, dehydrogenase, enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing guaiacyl-lignan content in monocotyledon plants, by transforming plant with chimeric gene construct having seed-specific transcriptional regulator linked to gene encoding protein involved in G-lignan formation
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Pred. No. 4.3e-26;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 SNSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMF
                                                                                                                                                                                                  Secoisolariciresinol dehydrogenase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON STATE RES FOUND. (PHYT-) APPLIED PHYTOLOGICS INC.
                                                              AAO21494 standard; Protein; 276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY54415 standard; Protein; 277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 10; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-SEP-2001; 2001WO-US27500.
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                                                                                                                                                       15-AUG-2002 · (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  relating to the invention.
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-425767/45.
N-PSDB; AAL38432.
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                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                         AA021494;
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Indels

AAYS4415
ID AAYS
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AC AAYS
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DT 06-A
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XX

RESULT 7

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06-SEP-2000
The present sequence represents a peptide of a secoisolariciresinol dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require nucleic acids are used for the secoisolariciresinol dehydrogenase in plants or to alter lignan secoisolariciresinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase active lignan, matairesinol. The secoisolariciresinol dehydrogenase alter the lavels of health-protecting lignans, including phytoestrogens such as enterolactone and enterodiol, in plant species, including cause and treated plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutricenticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of poptically pure lignans having desirable bloogical properties, and (-)-podophyllotoxin.
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                                                                                                                                                                                                                   New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 37910.
(-)-trachelogenin; antiviral; (-)-podophyllotoxin.
                                                                                                                                              (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                      Xia Z, Costa MA, Davin LB, Lewis NG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG31552 standard; Protein; 283 AA.
                                                                                                                                                                                                                                                        Example 1; Page 58; 66pp; English.
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                                                                                               99WO-US08975.
                                                                                                                       98US-0082977.
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                      Forsythia intermedia.
                                                                                                                                                                                              WPI; 2000-126356/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17 AA;
                                                                                               23-APR-1999;
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                                                WO9955846-A1.
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AAG31552
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990S-0131449.
990S-0132048.
990S-0132407.
990S-0132484.
990S-0132485.
                                    99US-0123180.
99US-0123548.
99US-0126264.
99US-0126785.
99US-0127462.
99US-0127462.
25-FEB-2000; 2000EP-0301439
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990S-0142055.
990S-0142059.
990S-0142803.
990S-0142803.
990S-014324.
990S-0144325.
990S-0144333.
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.00.0%; Pred. No. 1.1e-07;
.ve 0; Mismatches 0;
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Best Local Similarity 100.0%; P:
Matches 16; Conservative 0;
                           990S - 0156458

990S - 0156596

990S - 0156596

990S - 0157753

990S - 0158029

990S - 0158029

990S - 0158029

990S - 0159293

990S - 0159293

990S - 0159293

990S - 0159330

990S - 0159330

990S - 0159331

990S - 0159331

990S - 0160741

990S - 0160767

990S - 0160814

990S - 0161405

990S - 0161405

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990S - 0161360

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99US-0155139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
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                                                                                                                                                                      Claim 5; SEQ ID NO 2034; 261pp + Sequence Listing; English.
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Best Local Similarity 100.0%; Pred. No. 1.1e-07;
Matches 16; Conservative 0; Mismatches 0;
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99US -0123180
99US -012318
99US -012578
99US -012678
99US -012678
99US -012824
99US -012814
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99US -013049
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  Tietjen K, Weidler M;
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                                    WPI; 2002-269010/31.
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05-MAR-1999;
23-MAR-1999;
23-MAR-1999;
29-MAR-1999;
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08-APR-1999;
08-APR-1999;
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27-APR-1999;
28-APR-1999;
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AAG18620
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AAG18620
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990S-0132486.
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990S-0134218.
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Gaps

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Length 300; Indels

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                         1.2e-07;
                                                                                                                                                                                                                                      5.9%; Score 16; DB 21;
llarity 100.0%; Pred. No. 1.2e-07
Conservative 0; Mismatches 0
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                  99US-0160815.
99US-0160980.
99US-0160981.
99US-0161404.
99US-0161405.
99US-0161360.
99US-0161359.
99US-0161359.
99US-0161361.
99US-0161361.
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99US-0123180.
99US-0125788.
99US-0125788.
99US-0126745.
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99US-0126785.
99US-0126785.
99US-01267874.
99US-0130077.
99US-0130081.
99US-01308845.
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99US-0131449.
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Les 16; Conserv
                   21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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01-APR-1999;
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19-APR-1999;
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Best Local S
Matches 16
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12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
13-AUG-1999;
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7-7UL-1999 8-7UL-1999 8-7UL-1999 2-AUG-1999 2-AUG-1999 4-AUG-1999 6-AUG-1999 6-AUG-1999 6-AUG-1999	9-AUG-199 10-AUG-199 11-AUG-199 22-AUG-199 23-AUG-199 6-AUG-199 10	15. SEP-1999 16. SEP-1999 22. SEP-1999 23. SEP-1999 24. SEP-1999 24. SEP-1999 26. OCT-1999 06. OCT-1999 07. OCT-1999 13. OCT-1999 14. OCT-1999 14. OCT-1999 14. OCT-1999 14. OCT-1999 14. OCT-1999 14. OCT-1999 16. OCT-1999 17. OCT-1999 18. OCT-1999 19. OCT-1999 21. OCT-1999 22. OCT-1999 22. OCT-1999 23. OCT-1999 22. OCT-1999 23. OCT-1999 23. OCT-1999 24. OCT-1999 25. OCT-1999 25. OCT-1999 25. OCT-1999 25. OCT-1999
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New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
                                                                                                                           Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan; matairealnol; health-protecting lignan; phytoestrogen; enterolactone; enterolactone; enterolactone; enterolactone; enterolactone; contini antiviral; (-)-todophyllotoxin.
                                                                                                      Trypsin fragment of a secoisolariciresinol dehydrogenase protein.
                                                                                                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                    AAY54419 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 58; 66pp; English.
                                                                                                                                                                                                                                                                                                                        Costa MA, Davin LB,
                                                                               06-APR-2000 (first entry)
                                                                                                                                                                                   Forsythia intermedia.
                                                                                                                                                                                                                                                                                                                                             WPI; 2000-126356/11.
                                                                                                                                                                                                       WO9955846-A1
                                                                                                                                                                                                                                                     23-APR-1999;
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                                                          AAY54419;
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                 RESULT 14
                            AAY54419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
                                                                                                                             Gaps
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0
                                                                                                    Length 343;
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                                                                                                                           0; Indels
                                                                                                   Score 16; DB 21; I
Pred. No. 1.4e-07;
0; Mismatches 0;
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100.0%; Pred. No. 1.2e-05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                             Herbicidally active polypeptide SEQ ID NO 1660.
                                                                                                                                                                                                                                                                                                                    Herbicidal; plant; agriculture; herbicide.
                                                                                                                                                                                                                            ABB92449 standard; Protein; 280 AA
                                                                                                   5.3°,
100.0%; Pre-
99US-0161406.
99US-0161359.
99US-0161360.
99US-0161361.
99US-0161920.
99US-0161993.
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                                                                                                                                                             28-AUG-2001; 2001WO-EP09892.
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                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                11 LEGKVALITGGASGIG
                                                                                                                          16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tietjen K, Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as herbicides.
                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                WO200210210-A2.
                                                                                                                                                                                                                                                                        31-MAY-2002
                                   26-OCT-1999
                                            28-OCT-1999;
                       26-OCT-1999
                                                                             29-0CT-1999
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                                                                    28-OCT-1999
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ABB92449
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Lewis NG;

99WO-US08975.

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The present sequence represents a peptide of a secoisolariciresinol dehydrogenase. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require conclain acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of the enzymes. It is also used to obtain expression or enhanced expression of blosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase of proteins and nucleic acids can be utilized to: elevate or otherwise catler the levels of health-protecting lignans, including phytroestrogens such as enterolactone and enteroclain, in plant species including can be utilized to: elevate or otherwise such genetically altered blants; genetically altered plants; genetically altered from such genetically altered blants; genetically alter plant capecies to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriceuticals and dietary compundant supply of optically pure lignans having desirable biological componenties, for example (-)-trachelogenin which possesses antivital) componenties, and (-)-podophyllotoxin.
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nes 12; Conserv
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Conservative

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Query Match
4.0%; Score 11; DB 23; Length 127;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 0; Indels
                                               WO200192523-A2.
                                          Homo sapiens.
                                                    06-DEC-2001.
                                                                                                                                                                             Sequence
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The present invention describes substantially purified human proteins (referred to as open reading frame, OREX, where X is 1-11491 (see Table 1 in the specification) ABN15762 to ABN27352 encode the human OREX in the specification) ABN15762 to ABN27352 encode the human OREX recting given in ABP00010 to ABP11500. OREX proteins are useful for treating a pathology associated with an OREX-associated disorder. OREX polynucleotide syndrome associated with OREX-associated disorder. OREX polynucleotide sequences can be used in gene therapy. OREX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriamis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus systemic clupus extythematosus, hypertension, prycthyroidism, cholesterol ester storage disease, various immune disorders and disorders, infectious disease, autorimmune disorders such as multiple sclerosis, rheumatoid arthritis, autorimmune disorders such as multiple sclerosis, rheumatoid arthritis, autorimmune inflammatory eye disease. OREX proteins are also consensed and autorimmune inflammatory eye disease. OREX proteins are also bone degenerative disorders, or lorest fibrosis, consection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.

CN DES The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperpoliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                              Disclosure; SEQ ID 1076; 1037pp; English.
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Gaps

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233 ANAALYLASDE 243

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Human, open reading frame, ORFX, gene therapy, cancer; cirrhosis, hyperprofiferative disorder; psortiasis; benign tumour; hemorrhadge, degenerative disorder; psortiasis; benign tumour; hemorrhadge, carditovascular disease, diabetes mellitus; systemic lupus erythematosus; hypertenaton; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                         Human ORFX protein sequence SEQ ID NO:1076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
25-JUN-2002 (first entry)
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N-PSDB; ABN16299.
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17933, 7
21640, A
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316, Appl
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4148, Ap
66, Appl
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3894, Ap
19, Appl
180, App
17376, A
180, App
24819, A
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US-09-252-991A-19538
US-09-330-095-1
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US-09-252-991A-17933
US-09-252-991A-21640
US-09-457-040B-26
US-08-684-922A-38
US-08-684-922A-38
US-08-053-171-31
US-08-053-171-31
US-08-637-759B-454
US-08-637-759B-454
US-08-817-159B-454
US-09-201-945-454
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US-08-630-822A-66
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US-09-171-156A-25
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US-08-981-793A-618
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US-08-371-505-2
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19626, A
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APPLICANT: Susan E. Jensen

APPLICANT: Anish S. Paradkar

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic

PRECH NO. 6232106

TITLE OF INVENTION: Acid Biosynthesis

NUMBER OF SEQUENCES: 25

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CONDITES: IBM PC compatible

COMPUTER: IBM PC compatible

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US-09-312-283C-422
US-08-311-7314-334
US-08-466-886-40
US-08-466-886-40
US-08-469-617-40
US-09-220-528-53
US-09-1298-452A-1158
US-09-1298-452A-1158
US-09-1298-452A-1158
US-09-1298-452A-1158
US-09-127-492-37
US-08-577-492-37
US-09-128-352-822
US-09-328-352-822
US-09-311-328-2
US-09-311-328-2
US-09-511-328-3
US-09-511-358-3
US-09-515-388-3
US-09-515-388-3
US-09-515-388-3
US-09-515-388-3
US-09-107-532A-61837
US-09-107-532A-61837
US-09-107-532A-61837
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CLASSIFICATION:

PILING DATE:

CLASSIFICATION:

PRIOR PAPLICATION DATA:

APPLICATION NUMBER: US 08/790,462

FILING DATE: 29-7M-1997

ATOMNE: D. DOUGLAS FICE

REGISTRATION NUMBER: 24,514

RETERENCE/DOCKET NUMBER: 1418/P574521

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (202) 33905350

TELEFAX: RCA 248591 IDEA UR

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 248 amino acids

TYPE: a
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Sequence 11, Application US/09726614

Parent No. 6314735

GRAPPLOANT: Susan B. Jensen

APPLICANT: Susan B. Jensen

APPLICANT: Mashish S. Paradkar

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic

APPLICANT: Mashish S. Paradkar

TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic

TITLE OF INVENTION: Acid Biosynthesis

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS:

ADDRESSEE: JACOSGON, PRICE, HOLMAN & STERN, PPLC

STATE: D.C.

CONFURY: US A.A.

STATE: D.C.

COMPURY: US A.A.

COMPURY: BRADCASTON: PRED PROBENTIAL POLYAN COMPURE: INDEX COMPURE
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                                                                                                                                      Length 248;
                                                                                                                                                                                                                0; Indels
                                                                                                                                      Query Match
2.9%; Score 8; DB 3;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches
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US-09-328-352-5742
; Sequence 5742, Application US/09328352
; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-385-028-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / MOLECULE TYPE: protein US-09-726-614-11
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US-09-726-614-11
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                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 8; DB 3;
                                                                                               2.9%; Score 8; DB 4
100.0%; Pred. No. 7.9
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09026482B; Patent No. 614338; GENERAL INFORMATION: APPLICANT: SOWMENVILLE, CHRISTILLE OF INVENTION: ACYL-COA REDUCTASE; NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: DEPARTMENT OF ENERGY ADDRESSEE: GC 2 (FORSTL) MS-6F-067; STREET: 1000 INDEPENDENCE AVE. S.W. CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLIANCE THE P. CONTAILED CORRATIONS OPERATING SYSTEM: MS-DOS SOFTWARE: WORDDERFECT 6.22 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,482B FILING DATE: 02/19/98
ATTORNEY/AGENT INFORMATION:
NAME: ALMAN, JOY
REGISTRATION NUMBER: 40486
REFERENCE/DOCKET NUMBER: S-87814
TELECOMMUNICATION: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
                              ORGANISM: Staphylococcus epidermidis US-09-134-001C-4339
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GENERAL INFORMATION:
APPLICANT: Yoshihisa, Kasukabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Yoshihisa, Kasukabe
APPLICANT: Koichi, Fujisawa
APPLICANT: Susumu, Nishiguchi
APPLICANT: Yoshihiko, Maekawa
APPLICANT: Randy, Allen
TITLE OF INVENTION: COTTON FIBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: FLOPPY DISK COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%;
Best Local Similarity 100.0%;
                                                                                             Query Match
Best Local Similarity 100.
Matches 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                      14 KVALITGG 21
                                                                                                                                                                                                                                  46 KVALITGG 53
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US-08-580-545B-2
           TYPE: PRT
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Batent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-10-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 4339
LENGTH: 290
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 262
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE DE INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19626
LENGTH: 267
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Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches
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Pred. No.
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Patent No. 6551795
                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5742
                                                                                                                                                                                                                                                                                                                                            Query Match 2.9%; Scc
Best Local Similarity 100.0%; Pr
Matches 8; Conservative 0;
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ORGANISM: Pseudomonas aeruginosa
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18 GKVALITG 25
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US-09-328-352-4279
US-09-328-352-4279
Sequence 4279. Application US/09328352
Patent No. 656.298
GENERAL INFORMATION:
APPLICANT: GATY D. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: GTC99-0378
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 87
LENGTH: 87
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105-09-252-991A-21618

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100.0%; Pred. No. 25;
iive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                        Query Match 2.9%; Score 8; DB 3; Best Local Similarity 100.0%; Pred. No. 8.7; Matches 8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Acinetobacter baumannii
US-09-328-352-4279
TELECOMMUNICATION INFORMATION:
TELEPRONE: 202/783-5370
TELEPRAX: 202/783-231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-262-653A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa US-09-252-991A-21618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.6
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                         CITY: Washington
COUNTY: Washington
COUNTY: USA
COUNTY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
CORPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/580,545B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/262,653A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%; Score 8; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.7;
Best Ches 8; Conservative 0; Mismatches
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NAME: Breteschneider: Barry E.
REGISTREATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/068001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04473/068001
      NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 601 Thirteenth Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
ATTONEY/CAGENT INFORMATION:
NAME: Bretschneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04473/C
TELECOWMUNICATION INFORMATION:
TELERHONE: 202/783-5070
TELERHONE: 202/783-5070
TELERFAX: 202/783-2331
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 323 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-580-545B-2
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40 TGGASGIG 47
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US-09-262-653A-2
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Sequence 3, Application US/08815225

Patent No. 6268479

GENERAL INFORMATION:
APPLICANT: Stern, David M.
APPLICANT: Yan, Shi Du
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: GOODER & Dunham LLP
                      APPLICANT: Yan, Shi Du
TITLE OF INVENTION: AN INTRACELLULAR AMYLOID-BETA PEPTIDE
TITLE OF INVENTION: BINDING (ERAB) POLYPEPTIDE AND METHODS FOR INHIBITING
TITLE OF INVENTION: NEURODEGENRATIVE CONDITIONS
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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ZIP: 10036
COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225
FILING DATE: 12-MAR-1997
CLASSIFICATION: 536
ATTONNEY/AGENT INFORMATION:
NAME: White, 20hn P.
REGISTRATION NUMBER: 28,678
REPREBUCE/DOCKET NUMBER: 0575/55209
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1991-0525
INFORMATION FOR SEQ ID NO: 2:
GENTING CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,225 FILING DATE: 12-MAR-1997 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                      ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: NY YORK
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.6%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
  David M.
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amino acid
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      Stern,
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18834
LENGTH: 175
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Sequence 20, Application US/09648004

Patent No. 6498242

GABERAL INPORMATION:

APPLICANT: THOMAS, STUART

APPLICANT: NAGARAJAN, WASANTHA

TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND

TITLE OF INVENTION: INTERMEDIATES

FILE REPRESENCE: CL-1341-A

CURRENT APPLICATION NUMBER: 09/252,553

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 199-02-19

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Microsoft Office 97
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100.0%; Pred. No. 47;
iive 0; Mismatches
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                                                                                                                                                    Sequence 18834, Application US/09252991A
Patent No. 6551795
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US-08-815-225-2
; Sequence 2, Application US/08815225
; Patent No. 6266479
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.6%; Best Local Similarity 100.0%; Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Acinetobacter sp.
US-09-648-004-20
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Best Local Similarity 100...
7; Conservative
176 LAVELGQ 182
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                                         47 LAVELGO 53
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US-09-648-004-20
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LENGTH: 251
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US-09-347-878-50
US-09-347-878-50

Paguence 50, Application US/09347878C

Patent No. 6376210

GENERAL INFORMATION:

APPLICANT: Yind Chong

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES

CURRENT APPLICATION NUMBER: US/09/347,878C

UNMERN OF FLING DATE: 1999-07-06

NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0

ERNGTH 261

LENGTH 261

LENGTH 261
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2.6%; Score 7; DB 4; Length 261;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/55209

TELEFONNICATION INFORMATION:

TELEFONNE: (212) 278-0400

TELEFONNE: (212) 391-0525

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 261 amino acids

TENGTH: 261 amino acids

TENGTH: 261 amino acids

TENGTH: 261 amino acids

TYPE: amino aci
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; ORGANISM: Homo sapiens
US-09-347-878-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 ITGGASG 24
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Scoring table:

score:

Title: Perfect :

Sequence:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database

0

Word size

Searched:

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Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 23, Appli
Sequence 23, Appli
Sequence 11860, Appli
Sequence 111310, A
Sequence 11310, A
Sequence 11310, A
Sequence 11343, A
Sequence 11447, A
Sequence 20, Appli
Sequence 20, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 56, Appli
Sequence 56, Appli
Sequence 56, Appli
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Sequence 56, Appli
Sequence 60, Appli
Sequence 60, Appli
Sequence 61, Appli
Sequence 61, Appli
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Sequence 324, Appli
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Sequence 61, Appli
Sequence 21, Appli
Sequence 221, Appli
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Sequence 221, Appli
Sequence 231, Appli
Sequence 23, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence Sequence
2 US-09-882-227-180
US-09-765-272-180
US-09-738-626-6243
US-09-738-626-6243
US-09-864-761-38565
US-09-864-761-46287
S US-10-203-224-10
5 US-10-147-9518-1
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SS-10-208-021-360 SS-10-208-021-360 SS-10-208-026-360 SS-10-208-026-360 SS-10-208-029-360 SS-10-015-393A-336	S-10-232-2 S-10-195-8 S-10-196-7 S-10-015-8	S-10-174- S-10-175- S-10-175-	S-10-176 S-10-184 S-10-187	S-10-19 S-10-19 S-10-19	S-10-19	S-10-2 S-10-2 S-10-2	S-10-2	S-10-3	S-10-2 S-10-1	S-10-1 S-10-2	S-10-1 S-10-0 S-10-0	S-10-0	S-10-1	S-10-(S-10-1	S-10-1	S-10-3	S-10-	S-10-1	S-10-3	S-10-3	S-10-0 S-10-0	S-10-0	S-10-2	S-10-1 S-10-1	8-10-1	S-10-1	S-10-1 S-10-1	S-10-19 S-10-20	S-10-20	S-10-20
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US-10-242-505-82 US-10-242-574-82)-243-261-8)-243-282-8	0-243-402-8)-243-431-8)-245-164-8	0-244-972-8)-197-942-8)-238-196-8	0-245-013-8	0-245-103-8)-245-107-8)-245-143-6)-245-771-8	0-245-851-8	0-245-883-8)-237-535-8 -236-163-6)-238-183-8)-238-283-8	1-238-370-8)-245-055-8 -245-147-8	0-245-730-8	0-245-739-8)-246-210-8)-239-196-8	0-243-024-8	0-243-409-8)-245-621-8)-245-880-8	0-245-033-8	0-243-095-8	0-245-185-8)-245-42/-8)-245-473-8	0-245-770-8)-245-877-8)-246-976-8	1-243-320-8	0-242-743-8)-242-845-8)-237-636-8	0-238-325-8	0-238-346-8)-243-124-8)-243-124-8	0-243-425-8)-245-874-8)-245-874-8	0-242-653-8)-243-167-8)-243-388-8	0-244-947-8	0-244-968-8)-245-079-8)-245-079-8	0-245-127-8	0-245-207-8)-245-695-8)-245-695-8	0-245-699-8)-245-737-8)-245-890-8	1-245-899-8	0-245-900-8)-247-058-8)-245-454-8	0-237-471-8)-238-261-8)-238-324-8	0-241-860-8
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Sequence 182, App Sequence 182	11821, 1821, 1821, 1821, 1821, 1821, 1821, 1821, 1821, 1821,
US-10-143-030A-303 US-10-1943-030A-303 US-10-194-457-182 US-10-194-457-182 US-10-194-457-182 US-10-194-457-182 US-10-196-477-182 US-10-173-699-182 US-10-173-699-182 US-10-173-699-182 US-10-173-699-182 US-10-173-699-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-174-589-182 US-10-175-744-182 US-10-175-744-182 US-10-175-744-182 US-10-175-744-182 US-10-175-744-182 US-10-175-744-182 US-10-176-789-182 US-10-176-789-182 US-10-176-789-182 US-10-176-789-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-176-924-182 US-10-177-191-313 US-10-177-191-313 US-10-177-486-182 US-10-177-486-182 US-10-177-486-182 US-10-177-698-182 US-10-176-981-182	US-10-1 US-10-1 US-10-1 US-10-2 US-10-2 US-10-2 US-10-1 US-10-
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2.9%; Score 8; DB 15; Length 251;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels
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63 SNSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMF 96
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Best Local Similarity 100.0%; Pred. No. 16;
Best Local Similarity 0, Mismatches 8; Conservative 0; Mismatches
                                                                                   RESULT 2
US-10-156-761-14812
Sequence 14812, Application US/10156761
Sequence 14812, Application US/10156761
Spublication No. US20030119018A1
GENERAL INCORMATION:
APPLICANT: OKURDA, HARUO
APPLICANT: SHIRAM, HIROSHI
APPLICANT: SHIRAM, HIROSHI
APPLICANT: APPLICANT: ADAVCSHI
APPLICANT: APPLICANT: ADAVCSHI
APPLICANT: APPLICANT: NOVEL POLYNUCLEOTIDES
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: JP 2001-204089
PRIOR PLILNG DATE: 2001-05-30
PRIOR PLILNG DATE: 2001-05-30
PRIOR PLILNG DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14812
LENGTH: 251
TYPE: PRI
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US-10-156-761-14537
Sequence 14537, Application US/10156761
SUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: HARTAWA, HROSHI
APPLICANT: HARTAWA, HROSHI
APPLICANT: HARTORI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYMUCEOTIDES
FILE REFERENCE: 249-262
CURRENT PALLICANION NOVEL POLYMUCEOTIDES
FILE REFERENCE: 249-262
CURRENT FILING DATE: 2002-05-29
FRIOR FILING DATE: 2001-05-30
FRIOR PELICATION NUMBER: JP 2001-204089
FRIOR FILING DATE: 2001-05-30
FRIOR PELICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14537
LIENGTH: 253
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-14537
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ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: secoisolariciresinol dehydrogenase amino acid
US-09-944-160-24
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US-09-944-160-24
Sequence 24, Application US/09944160
SETILGANT: Leavin, Laurence
APPLICANT: Devin, Laurence
TITLE OF INVENTION: Content
FILE REFERENCE: WGUI17983
CURRENT PILIOR DATE: 2001-08-30
SURRENT FILING DATE: 2001-08-30
PRIOR PELING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 24
LENGTH: 276
LENGTH: 276
LENGTH: 276
US-10-176-758-182
US-10-173-76-182
US-10-173-76-182
US-10-175-738-182
US-10-175-738-182
US-10-176-482-182
US-10-176-75-182
US-10-176-75-182
US-10-176-75-182
US-10-176-75-182
US-10-176-75-182
US-10-176-75-182
US-10-174-58-182
US-10-174-58-182
US-10-176-747-182
US-10-176-98-182
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FRIOR APPLICATION NUMBER: 09/154,707
FRIOR APPLICATION NUMBER: 09/154,707
FRIOR APPLICATION NUMBER: 09/154,707
FRIOR FILING DATE: 1998-03-19
FRIOR PRILING DATE: 1998-03-19
FRIOR FILING DATE: 1997-03-21
FRIOR PELICATION NUMBER: US 60/041,277
FRIOR APPLICATION NUMBER: US 60/041,374
FRIOR APPLICATION NUMBER: US 60/042,344
FRIOR APPLICATION NUMBER: US 60/042,344
FRIOR APPLICATION NUMBER: US 60/041,276
    Pred. No. 17;
                                              0; Mismatches
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PRIOR FILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-06-65
PRIOR PLING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR PLING DATE: 1997-10-02
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DR FILING DATE: 1997-05-30
DR APPLICATION NUMBER: US 60/048,186
DR FILING DATE: 1997-05-30
DR PLING DATE: 1997-05-30
DR PELING DATE: 1997-05-30
PR FILING DATE: 1997-05-30
PR FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,099
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,096
FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/041,281
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APPLICATION NUMBER: US 60/050,937
FILING DATE: 1997-05-30
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APPLICATION NUMBER: US 60/048,351
FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 128, Application US/09984245
Patent No. US20020165374A1
GENERAL INFORMATION:
Best Local Similarity 100.0%;
Matches 8; Conservative 0
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 128
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Publication No. US20030148324A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: I.N.S.E.R.M.

TITLE OF INVENTION:
FILE REPERENCE: BLANDINE: US/10/238,075

CURRENT APPLICATION NUMBER: US/10/238,075

CURRENT FILING DATE: 2002-09-10

PRIOR APPLICATION NUMBER: 0003145

PRIOR FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 15/6

SEQ ID NO 473

LENGTH: 268

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                                                                                                                                                                                                                                                                                             APPLICANT: HABSELDEAN, NUCELL
APPLICANT: Oblean, Karil
APPLICANT: Oblean, Karil
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
ITILE OF INVENTION: Prokaryotes
ITILE REFERENCE: ELITRA.011A
CURRENT FAILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLING DATE: 2000-05-25
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR PELING DATE: 2001-02-17
PRIOR PELING DATE: 2001-02-17
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100.0%; Pred. No
tive 0; Mismat
                                                                                                                                                         Sequence 10597, Application US/09815242 Patent No. US20020061569A1 GENERAL INFORMATION: APPLICANT: Haselbeck, Robert
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; ORGANISM: Enterococcus faecalis
US-09-815-242-10597
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Matches 8; Conservative
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GKVALITG 19
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                                                                                                                       US-09-815-242-10597
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TITLE OF INVENTION: 87 Human Secreted Proteins FILE OF INVENTION: 80 July 1940
CURRENT FILING DATE: 2030-10-29
RRIOR PELING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-17
PRIOR FILING DATE: 1998-09-17
PRIOR FILING DATE: 1997-03-21
PRIOR PILING DATE: 1997-03-21
PRIOR PELICATION NUMBER: US 60/041,276
PRIOR PELING DATE: 1997-03-21
PRIOR PELING DATE: 1997-05-30
PRIOR PELING DATE: 1997-
                                       60/060,862
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US-09-981-966-128
US-09-981-96-128
; Sequence 128, Application US/09983966
; Publication No. US20030060619A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 1997-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 128
LENGTH: 53
                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-966-262-128
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Publication No. US20030050461A1
APPLICANT: Young et al.
ITILE OF INVENTION: 87 Human Secreted Proteins
FILE REPRENATION: 80 Human Secreted Foots: 80 Human
   ; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-245-128
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US-10-291-190-45

Sequence 45, Application US/10291190

Sequence 45, Application US/10291190

Publication No. US20030171549A1

GENERAL INFORMATION:

APPLICANT: Structural Genomix, Inc.

APPLICANT: Buchanan, Sean Grant

APPLICANT: Buchanan, Sean Grant

APPLICANT: Sauder, J. Michael

TITLE OF INVENTION: CRYSTALS AND STRUCTURES OF YIM PROTEINS

FILE REFERENCE: 52498-20009.00

CURRENT FILING DATE: 2002-11-08

PRIOR APPLICATION NUMBER: US 60/337,769

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 58

SSET ID NOS: 58
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APPLICANT: Conserved and Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: 12.1TRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
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                                                                                                                                                                                                                                                                         Length 92;
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o. 1:1e+02;
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                                                                                                                                                                                                                                                                                                                             0; Mismatches
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Best Local Similarity 100.0%; Pred. No.
Matches 7; Conservative 0; Mismatch
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; __LENGTH: 181
; TYPE: PRT
; ORGANISM: D. radiodurans (15806071)
US-10-291-190-45
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Matches 7; Conservative 0
                                      LENGTH: 92
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                        NAME/KEY: MISC_FEATURE LOCATION: (49)
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US-09-815-242-13753
          SEQ ID NO 4341
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                                                                                                                  FEATURE:
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Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2000-09-28
FRIOR APPLICATION NUMBER: US 60/157,137
FRIOR FILING DATE: 1999-09-29
FRIOR FILING DATE: 1999-09-29
FRIOR FILING DATE: 1999-11-03
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Publication No. US20030069406A1
GENERAL INFORMATION:
APPLICATY: Voung et al.
TITLE OF INVENTION: 87 Human Secreted Proteins
FILE REFERENCE: PZ004P1
CURRENT APPLICATION NUMBER: US/10/143,090
CURRENT FILING DATE: 2002-05-13
FRIOR APPLICATION NUMBER: 09/154,707
FRIOR APPLICATION NUMBER: 09/154,707
FRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
SSOTUM 128
PRIOR PILING DATE: 1997-05-30
PRIOR APPLICATION WUMBER: US 60/048,154
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-08-30
PRIOR PILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: US 60/056,370
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-19
PRIOR PILING DATE: 1997-08-10
PRIOR PILING DATE: 1997-11-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-143-090-128
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US-10-106-698-4341
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US-10-143-090-128
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Query Match 2.6%; Score 7; DB 15; Length 233 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 7; Conservative 0; Mismatches 0; Indels
        Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-9390

Sequence 9390, Application US/10156761

Publication No. US20030119018A1

GENERAL INFORMATION:

APPLICANT: OWURA, SATOSHI

APPLICANT: OKENATION:

APPLICANT: SHIRAMA, UNN

APPLICANT: SHIRAMA, HIROSHI

APPLICANT: SHIRAMA, HIROSHI

APPLICANT: ARHARVI TARAYOSHI

APPLICANT: HATTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REPERRENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT PLILOS DATE: 2002-05-29

PRIOR PLILONG DATE: 2001-05-30

PRIOR PLILONG DATE: 2001-05-30

PRIOR PLILONG DATE: 2001-05-30

PRIOR PLILON DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 15109

SEQ ID NO 9390

LEAGTH: 233
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                                                                                                            146 STASLSS 152
                                                                                                                                                                           131 STASLSS 137
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CURRENT APPLICATION NUMBER: US/09/811,284

CURRENT FILING DATE: 2001-03-16

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.6%; Score 7; DB 9; Length 199; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 7; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: Rate Salmonella typhi
US-09-815-242-13753
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CORGANISM: Homo sapiens
US-09-811-284-144
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98 PTALGKK 104
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Length 233;

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WS-10-272-419-20

WS-10-272-419-20

Sequence 20, Application US/10272419

Sequence 20, Application No. 1020303087403A1

Sequence 20, Application No. 1020303087403A1

SENDICATION NO. 10203

APPLICANT: CHOMAS, STUART

APPLICANT: HOMAS, STUART

APPLICANT: NAGARAJAN, VASANTHA

TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC AND

TITLE OF INVENTION: BIOLOGICAL METHOD FOR THE PRODUCTION OF ADIPIC ACID AND

TITLE OF INVENTION: WINDER: US/10/272,419

CURRENT FILING DATE: 1999-02-10-16

PRIOR APPLICANTON NUMBER: 09/252,553

PRIOR PELLING DATE: 1999-02-19

NUMBER OF SEQ ID NOS: 32

SOFTWARE: MICROSOFT OFFICE 97

LENGTH: 251
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2.6%; Score 7; DB 9; Length 204;

, * Query Match

12 KVALITG 18

Search completed: October 23, 2003, 13:15:07 Job time: 110 secs

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version 5.1.6 - 2003 Compugen Ltd.	model	:30 ; Search time 40 Seconds (without alignments) 656.351 Million cell updates/se	IDGGFSVCNSVIKVFQYPDS 273		esidues		parameters: 283308		summaries				predicted by chance to have a score of the result being printed	total score distribution.	SUMMARIES	Description		probable short probable alcoho	probable short	glucose I-deny 2-deoxy-D-gluco	hypothetical pi toluenesulfonat	hypothetical pi	preridine	probable alcom probable alcoh	oxidoreductase 3-oxoacv1-(acv	3-oxoacyl-(acy	glucose 1-dehy	hypothetical pi alcohol dehydro	oxidoreductase	short-chain alo	sorbitol-6-pho: 2-deoxy-D-gluco	3-oxoacyl-[acy	promate 3-recoacy hypothetical prote probable dehydrone	
GenCore ver Copyright (c) 1993 - 2	OM protein - protein search, using sw mo	Run on: October 23, 2003, 12:59:	Title: US-09-673-918A-2 Perfect score: 273 Sequence: 1 MQLRTAFARRLEGKVALITG.	Scoring table: OLIGO Gapop 60.0 , Gapext 60.0	Searched: 283308 seqs, 96168682 re	Word size : 0	Total number of hits satisfying chosen p	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Listing first 1000 summ	PIR 76:	2: Direct.: 3: Direct.:	pir4	No. is the number of greater than or equal	ved by analysis of the	de	Result Query No. Score Match Length DB ID	17 6 2 234 2	17 6.2 284 2 16 5.9 283 2	13 4.8 267 2	10 3.7 255 2	10 3.7 256 2 10 3.7 262 2	10 3.7 285 2	9 3.3 245 2	9 3.3 258 2	9 3.3 258 2	9 3.3 259 2	9 3.3 272 2	9 3.3 275 2 9 3.3 286 2	9 3.3 287 2	33.33.33.23	9 3.3 689 2 8 2.9 158 2	8 2.9 240 2	28 8 2.9 252 2 B90495 29 8 2.9 253 1 S17711	

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hypothetical prote staphylokinase - p staphylokinase - p STAPHYLOKINASE PRE benzoate 1,2-dioxy beta protein homol related to H+tran ribosome releasing probable bacteriop hypothetical prote phypothetical prote hypothetical prote phypothetical prote phypothetical prote phypothetical prote probable regulator probable regulator probable populator probable protein protein protein probable protein protein protein protein protein protein protein protein probable protein protein protein protein protein protein protein hypothetical protein might protein might be protein xFG	ECF family sigma f MutThudix family conserved hypothet acetyltransferase hypothetical prote alkyl hydroperoxid unknown protein, 9 hypothetical prote hypothetical prote hypothetical prote phenylalanine-tRNA dephospho-CoA kina hypothetical prote probable membrane probhage pil prote probhage con-alcoh probable con-alcoh probable transerip glutathione transf hypothetical prote probable exported probable exported probable adenylate probable adenylate probable adenylate probable dihydroxy flagellin B1 precu transforming prote probable dihydroxy flagellin B2 precu transforming prote probable lexA prot probable lexA prot flagellin B1 precu myelin/oligodendro hypothetical prote probable prote probable prote probable phox! prot probable phox! prot probable phox! pro
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268 2 B4780 268 2 B90698 268 2 B90698 268 2 D85548 269 2 B22472 269 2 AE2285 269 2 F97308	2000 2000 2000 2000 2000 2000	272 273 273 273 273 273 273	273 273 273 20 20 20 20 20	22222	275 275 275 276 276	2772 2772 2772	277 2 278 1 279 2	281 281 281 281 281	282 1 282 1 283 1 283 1 2 8 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	283 2854 2854 285 285 285	286 286 286 286 286	2 2 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4	289 2 290 1 292 2	292 292 293 293 293	293 293 203 204	294 2 295 2 295 2	297 297 297 200	225. 2298. 2398. 2	3 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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3-oxoacy1-(acy1-ca probable short-cha thiamin biosynther thiamin biosynthes HesA protein (impo hypothetical prote short-chain dehydr	2-deoxy-D-glu 2-deoxy-D-glu cis-1,2-dihyd probable shor 2-deoxy-D-glu	probable (important) 2-keto-3-deoxhypothetical hypothetical	dehydrogenase 3 (or 17) beta- 3-oxoacyl-(ac short chain d	hypothetical hypothetical probable hist sorbitol util	tniamin blosy oxidoreductas enoyl-CoA hyd molybdopterin	probable shor probable dehy uncharecteriz	hypothetical hypothetical probable dehy expansin - up	ferredoxin-NADP+ ferredoxin-NADP r cis-1,2-dihydro-1	cls-1,2-dlnydro-1, dehydrogenase Atuf probable membrane conserved hypothet	hypothetical prote 3-hydroxyacyl-CoA probable fabd3 pro probable 3-oxoacyl	short-chain dehydr short-chain dehydr probable oxidoredu	probable crop 1,6-dihydroxy exodeoxyribon conserved hvo	ribosomal pro N-acetylmuram phenylacetic	HAD superfami 3-oxoacyl-(ac phosphorylati	hypothetical conserved hyp		thiamin biosy transcription	hypothetical prote cis-1,2-dihydro-1, hypothetical prote hypothetical prote	pre
2 D83766 2 F83098 2 H75123 2 AH1993 2 F81985 1 H96965																			
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probable UDPglucos inosine-uridine pr 3.dehydroquinate d hypothetical prote conserved hypothet probable sugar-bin probable sugar-bin probable sugar-bin probable sugar-bin probable sugar-bin probable sugar-bin ADPglyceromanno-he tryptophanyl-tRNA conserved hypothet succincglycan bios tryptophanyl-tRNA hypothetical prote tryptophanyl-tRNA moxR protein homol phosphate acetyltr conserved hypothetical prote hypothetical prote tryptophanyl-tRNA moxR protein lampol hypothetical prote tryptophanyl-tRNA moxR protein lampol hypothetical prote tryptophanyl-tRNA moxR protein lampol hypothetical prote hypothetical prote transforming prote sass protein lipoate probable cell cycl hypothetical prote oxidoreductase, sh flagellar m-ring p hypothetical prote bypothetical prote bypothetical prote transcription regu electron transfer hemagglutinin - in hemagglutinin - in hemagglutinin - in	hemagglutinin 1 - hypothetical prote probable trytophan rod shape-determin hemagglutinin 1 -
324 2 13954 2 13955 3 325 2 2 848272 3 848272 3 848272 3 848272 3 848272 3 848272 3 848282 2 848282 3	00000000000000000000
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2.2 348 2 A70311 2.2 349 2 14447 2.2 350 2 14447 2.2 350 2 14447 2.2 351 2 2 14447 2.2 351 2 2 14447 2.2 351 2 2 14447 2.2 351 2 A01333 2.2 353 2 A01333 2.2 354 2 2 A01333 2.2 355 2 A01333 2.2 356 2 A01333 2.2 357 2 A01333 2.2 377 2 A01333 2.2 377 2 A01323 2.2 377 2 A01333 2.2 377 2 A01323 2.2	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	66666666666666666666666666666666666666	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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Thu Oct 23 14:56:12 2003

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probable alcohol dehydrogenase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: H85039
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
R;anonymous, The European Union Arabidopsis of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: H8503
A;Accession: H8503
A;Accession: H8503
A;Accession: H8503
A;Accession: Basinanary
A;Accession: Basinanary
A;Accession: Afg03140
A;Accession: Afg
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C;Species: Vigna unguiculata (cowpea)
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000
C;Accession: T1199
A; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.
J. Plant Res. 109, 415-424, 1996
A;Riuchi, S.; Yamaguchi-Shinozaki, K.; Urao, T.; Shinozaki, K.
J. Plant Res. 109, 415-424, 1996
A;Reference number: 217293
A;Accession: T11579
A;Accession: T11570
A;Accession
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N;Alternate names: protein ipa-82d
N;Alternate names: protein ipa-82d
C;Contains: probable dehydrogenase (EC 1.1.1.-)
C;Species: Bacillus subtilis
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S39737; E70055
R;Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu,
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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4.8%; Score 13; DB 2; Length 267;
Best Local Similarity 100.0%; Pred. No. 3.1e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
     Length 284;
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5.9%; Score 16; DB 2; Length 283;
Best Local Similarity 100.0%; Pred. No. 2.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
Ouery Match
6.2%; Score 17; DB 2; Length 284
Best Local Similarity 100.0%; Pred. No. 2.38-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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NyAlternate names: TFHP-1 protein
Cispecies: Nicotiana tabacum (common tobacco)
Cispecies: Nicotiana tabacum (common tobacco)
Cipate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
Cipate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
Cipate: Nicotiana tabacum (common tobacco)
Cipate: Nicotiana tabacum (common tabacum)
A; Kawaoka, A.; Kawamoto, T.; Sekine, M.; Yoshida, K.; Takano, M.; Shinmyo, A.
A; Title A. cis-acting element and a trans-acting factor involved in the wound-induced ex A; Accession: T03734
A; Reference number: Z15039; MUID:95004656; PMID:7920706
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-234 < KAWA
A; Residues: 1-234 
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probable short chain alcohol dehydrogenase - common tobacco
c;Species: Nicotiana tabacum (common tobacco)
c;Date: 102257
C;Accession: T02257
C;Accession: T02257
C;Accession: T02257
C;Accession: T02257
C;Accession: T02257
A;Title: A simplified procedure for the subtractive cDNA cloning of photoassimilate-resp
A;Recence number: S62698; MUID:96145513; PMID:8555446
A;Accession: T02257
A;Accession: T02257
A;Residues: 1-284 A:RER>
A;Residues: 1-284 A:RER>
A;Residues: 1-284 A:RER>
A;Residues: 1-284 A:RER>
A;Csossion: T02257
A;Csossion
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probable replications
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T01500
T51929
D84340
D83622
T04944
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S69336
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A71649
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R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. B, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2307
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toluenesulfonate zinc-independent alcohol dehydrogenase [imported] - Brucella melitensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1.262 «KUR»
A;Cross-references: GB:AE008918; PIDN:AAL53525.1; PID:g17984431; GSPDB:GN00191
                                                                                                                                                                                                      Cispecies: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AD2307
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C,Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
                                                                                                                                                                               hypothetical protein alr4011 [imported] - Nostoc sp. (strain PCC 7120)
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100.0%; Pred. No. 0.039;
ive 0; Mismatches 0;
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Pred. No. 0.04;
); Mismatches
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Best Local Similarity 100.
Matches 10; Conservative
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Best Local Similarity 100.
Matches 10; Conservative
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LEGKVALITG 16
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2-deoxy-D-gluconate 3-dehydrogenase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: C87434
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, K.B.; Dankin, M.L.; Haft, D.H.; Kolon
N. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: C87434
A;Residues: 1-255 <STO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 17255 < KUN>
A; Residues: 17255 < KUN>
A; Cross-references: GB:299123; GB:AL009126; NID:g2636240; PIDN:CAB15799.1; PID:g2636308
A; Experimental source: strain 168
C; Genetics:
A; Gene: ywfD
C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C; Superfamily: ribitol dehydrogenase
C; Keywords: NAD; oxidoreductase
F; 8-185/Domain: short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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100.0%; Pred. No. 0.039;
tive 0; Mismatches 0; Indels
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A,Accession: E70055
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Pred. No. 0.039;
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Lircakscic 20 17 LITGGASGIG 26

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A; Molecule type: DNA

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10; Conservative

Matches

Best Local Similarity

Query Match

CC1492

C;Genetics:

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A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
A;Robidues: 1-257 «ROU»
A;Roberimental source: cultivar Columbia
A;Cross-references: EMBL:AC004411; NID:g3522932; PID:g3522935
A;Experimental source: cultivar Columbia
A; Kou, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., A;Ritis : Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB-AE002093; NID:g3522935; PIDN:AAC34217.1; GSPDB:GN00139
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. eubmitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme A;Authors: Macfaira, M.L.; Kemper, E.L.; Kitejima, J.P.; Kitejer, J.B.; Kuramae, E.E.; Ladgrechoo, M.A.; Madeira, A.M. B.N.; Madeira, H.M.; Manco, M.C.; Martuns, E.M.; Matthors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Wunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; G. Rosa, M.C.; Palmideri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, K.G.; Santelli, R.V.; Sawaeash A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvairâ, M.; Tenhanda, M.H.; Vallada, H.; Vallada, H.; Vallada, H.; Vallada, M.S.; Verfoveki-Almeida, S.; Vettore, A.L.; Za A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: XF1457
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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2021/6
probable alcohol dehydrogenase At2g47120 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F14M4.5
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Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
3.3%; Score 9; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches
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A;Map position: 2
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B18260

pteridine reductase 1 XF1457 [imported] - Xylella fastidiosa (strain 9a5c)
c;Species: Xylella fastidiosa
c;Species: Xylella fastidiosa
c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C;Accession: B8260
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent Aintle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59128 below
A;Scatus: preliminary
A;Notecule type: DNA
A;Residues: 1-245 <SIN>A;Residues: 1-245 <SINAAFB4266.1; GSPDB:GNOO1A;Resimental source: strain 95c
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bphB protein - Comamonas testosteroni (fragment)
bphB protein - Comamonas testosteroni (fragment)
C;Species: Comamonas testosteroni
C;Species: Comamonas testosteroni
C;Species: T7-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 08-Oct-1999
C;Accession: PC4213
R;Sylvestre, M.; Sirois, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria
Gene 174, 195-202, 1996
A;Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl dioxy
A;Recension: PC4213
A;Molecule type: DNA
A;Residues: 115 < SYL>
A;Residues: 115 < SYL>
A;Cross references: GB:U47637; NID:g1245151; PIDN:AAC44530.1; PID:g1245156
C;Genetics: A;Genetics: A;G
            ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A.Reference number: A86141; MUID:21016719; PMID:11130712

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-285 <STC>
A.Residues: 1-286 <STC>
A.Residues: 1-288 <STC>
A.Residues:
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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3.3%; Score 9; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels
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Matches 10
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oxoacyl-(acyl-carrier protein) reductase [imported] - Agrobacterium tumefaciens (strai,
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A;Molecule type: DNA
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02176; C84911
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
                                                                                                                                                                                                                                                           Accession: C84911
Accession: C8411
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Accession: C84911
Accession: C84911
Accession: C84911
Accession: C84911
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H75616
Oxidoreductase, short-chain dehydrogenase/reductase family - Deinococcus radiodurans (st
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C;Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: H75616
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma Science 286, 1571-1577, 1999
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A;Experimental source: strain R1
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A;Cross-references: GB:AE002093; NID:g3522936; PIDN:AAC34218.1; GSPDB:GN00139
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A,Molecule type: DNA
A,Residues: 1-258 <ROU>
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A,Map position: 2
A,Introns: 5/2
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RESULT 15

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C;Accession: A13149
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. R;Wood, D.W.; Setubal, Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                             ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A13149
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Cross-references: GB:AE008689; PIDN:AAL45615.1; PID:g17743336; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
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Best Local Similarity. 100.0%; Pred. No. 0.4
Matches 9; Conservative 0; Mismatches
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SECONDE FROM N.A.

MEDINE-9425297; PubMed=7515041;

Nagata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;

Nagata Y., Ohtomo R., Miyauchi K., Sukuda M., Yano K., Takagi M.;

Nagata Y., Ohtomo R., Miyauchi K., Sukuda M., Yano K., Takagi M.;

Glohing and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohexane in Pseudomonas paucimobilis.";

J. Bacteriol. 176:3117-3125(1994).

-!- FUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL
(2,5-DDOL) INTO 2,5-DICHLOROHYDROQUINONE (2,5-DCHQ). LINX IS NOT
ESSENTIAL TO GAMMA-HCH DEGRADATION.

-!- PATHWAY: Degradation of gamma-hexachlorocyclohexane.

-!- SATHWAY: Degradation of gamma-hexachlorocyclohexane.

-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LINX PSEPA STANDARD; PRT; 250 AA.
950198;
90101-1996 (Rel. 34, Created)
10-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.)
LINX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Protecobacteria; Alphaprotecobacteria; Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
NCBI_TaxID=13689;
QBuj69
QBpnr3
QBpnr3
QBpnr3
Pb 7526
Pb 74748
QOS 8819
QOS 8819
QOS 8819
QOS 8819
Po 8819
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PRINTS; PRO00080; SDRPAMILY.
PROSITE; PS00061; ADH SHORT; 1.
Aromatic hydrocarbons carabolism; Oxidoreductase; NAD.
NP BIND 9 34 NAD (BY SIMILARITY).
ACT SITE 156 BY SIMILARITY.
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RS8 XANCE
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Y426 MYCGE
Y426 MYCGE
Y067 CABEL
CRB2 BACHD
CYB ANOCU
NRDI YBRPE
NRDI YBRPE
NRDI YBRPE
NRDI YBRPE
NRDI AGRE
VOS VARV
H3 AGRE
H3 EUPCR
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       FROM N.A.
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TINX PSEPA
       InterPro;
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DB 1; Length 250;

4.4%; Score 12;

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The Buropean Bioinformatics Institute are no restrictions on its use by non-profit institutions as long as its content is in no way
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Azevedo V., Bertero NG., Bessieres P., Bolotin A., Borchert S.,
Bar Azevedo V., Bertero MG., Bessieres P., Bolotin A., Borchert S.,
BA Azevedo V., Bertero MG., Bessieres P., Bolotin A., Borchert S.,
BA Borriss R., Boursier L., Brans A., Braun M., Brighnell S.C., Bron. B.
Bruillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
BR Brouillet S., Bruschi C.V., Connerton I.F., Cummings N.J., Daniel R.A.
Britz C., Evilta W., Fulita Y., Ferrari E., Foulger D.,
BR Entian K.D., Errington J., Padret C., Ferrari E., Foulger D.,
BR Ghim S.Y., Glaser P., Goffeau A., Gollacht A., Gallacron N.,
BR Ghim S.Y., Glaser P., Goffeau A., Gollacht J., Grandi G.,
BR Hibert H., Holsappel S., Hasenda B., Harwood C.R., Henaut A.,
BR Hibert M., Rochter P., Koningstein G., Krogh S., Kumano M.,
BR Kurita K., Laydus A., Liu H., Masuda S., Manuel C., Medigue C.,
BR Kurita K., Laydus A., Liu H., Masuda S., Manuel C., Medigue C.,
BR Kurita K., Laydus A., Liu H., Masuda S., Manuel C., Medigue C.,
BR Kurita K., Laydus A., Liu H., Masuda S., Manuel C., Medigue C.,
BR Perscon E., Pujic P., Purnelle B., Rapoport G., Rey M., Rynolds S.,
BR Perscon E., Pujic P., Purnelle E., Rapoport G., Rey M., Rynolds S.,
BR Atseger M., Rivolte C., Rocha E., Roche B., Roche B., Roche B., Roche B., Roche B., Raporott G., Schleich S., Schleich S., Schleich S., Schleich S., Schleich S., Wadlar H., Waitzenegger T.,
BR Akeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Togantott M., Wandner P., Vasunotoc M., Wandner P., Wanters P., Winpat A., Yamanoco H., Waitzenegger T.,
BR Winters P., Winpat A., Yamanoco H., Waitzenegger T.,
Britters P., Winpat A., Yamanoco H., Wamane K., Yasunotoc K., Yasunoco H., Wanters P., Winpat A., Yamanoco H., Wamane C., Woolker E., Yoshikawa H., Danchin A.,
Britters P., Winpat A., Yamanoco H., Wamane K., Yasunoco K., Wari A., Yasun K., Wanterin Bacillus R., Schleich S., Wedler E., Wedler H., Weitzenegger T.,
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-!- SIMILMSTRY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=168)
MEDILINE=595020337; PubMed=7934828;
MEDILINE=595020337; PubMed=7934828;
MEDILINE=595020337; PubMed=7934828;
MUILO M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,
Presecon E., Santana M., Schneider E., Schweizer J., Vertes A.,
Rapoport G., Danchin A.,
"Bacillus subfilis genome project: cloning and sequencing of the & bregion from 325 degrees to 333 degrees.";
Mol. Microbiol. 10:371-384(1993).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEB-1903 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase ywfD (EC 1.-.-).
YWFD OR IPA-82D.
Bacillus subtilis.
Bacteria, Firmitutes; Bacillales; Bacillaceae; Bacillus.
                      0; Indels
100.0%; Pred. No. 0.00024;
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                       13 GKVALITGGASG 24
                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                               BACSU
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YWFD_BACSU
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us-09-673-918a-2.oligo.rsp

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COMTE
  ACT SITE
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                                       Query Match
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                                                                                                                                                                    BPHB_COMTE
                                                               Matches
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  and for commercial
             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochim. Biophys. Acta 1350:317-324(1997).
-!- CATALYTIC ACTIVITY: ($)-3-hydroxyacyl-CoA + NAD(+) = 3-oxoacyl-CoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotetramer (By similarity).
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota, Metazoa; Chordata; Czaniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97214648; PubMed=9061028; Furuta S., Kobayashi A., Miyazawa S., Hashimoto T.; "Cloning and expression of cDNA for a newly identified isozyme of bovine liver 3-hydroxyacyl-CoA dehydrogenase and its import into
                                                                                                                                                                                                                                                        ö
                                           EMBL; X77124; CAA51638.1; -.

EMBL; Z99123; CAB15799.1; -.

PIR; S39737; S39737.

HSSP; P50162; J8737.

InterPro; IRR002198; ywfD.

PEAM; PF00106; add short; 1.

PRINTS; PR00080; SDRFAMILY.

PROSITE; PS00061; ADH SHORT; 1.

PROSITE; PS00061; ADH SHORT; 1.
                                                                                                                                                                                                                            3.7%; Score 10; DB 1; Length 255; 100.0%; Pred. No. 0.025; ive 0; Mismatches 0; Indels
  Usage by
                                                                                                                                                                                                     20AA2259BFB88C9B CRC64;
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modified and this statement is not removed. entities requires a license agreement (See hi or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PR051TE; PS00061; ADH SHORT; 1.
Oxidoreductase; NAD; Mitochondrion.
NP_BIND 12 NAD (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB002156; BAA19510.1; -.
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                                                                                                                                                                                         154 154 E
255 AA; 27324 MW;
                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                              17 LITGGASGIG 26
                                                                                                                                                                                                                                                                                                       11 Lirégaséie 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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SEQUENCE
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                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: Homotetramer.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
                                                                                                                                                                                                                                                                                                                                                                                                             Q463B1, Q46376;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3 1.56)

dihydroxybiphenyl dehydrogenase (EC 3.3-dihydro-2,3-dihydrocyphenyl-dis-dihydrocyphenyl-dehydrogenase)

(2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase) (B2,3D)
                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comamonas testosteroni (Pseudomonas testosteroni).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                 Length 261;
                                                                              3.7%; Score 10; DB 1; Length 261
100.0%; Pred. No. 0.026;
tive 0; Mismatches 0; Indels
BY SIMILARITY.
8C7572B6A9A49780 CRC64;
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InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00006; SDFFAMILY.
PROSTITE; P8000061; ADH_SHORT; 1.
Aromatic hydrocarbons catabolism; Oxidoreductage; NAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                            281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97045812; PubMed=8890734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96316386; PubMed=8702262;
                          27140 MW;
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NCBI_TaxID=285;
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                                                                                                                                     10; Conservative
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                       261 AA;
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REDINE=98044033; PubMed=9384377;

Runst F., Ogasswara N., Moszer I., Albertini A.M., Alloni G.,

Raevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boursier L., Braun A., Braun M., Brignell S.C., Bron S.,

Roriss R., Enuschi C.V., Caldadl B., Capuano V., Carter N.M.,

Robiss R., Enuschi C.V., Candadl B., Capuano V., Canter N.M.,

Robiss R., Errington J., Fabret C., Ferrari E., Foulger D.,

Rantian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Rantian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

Rantian K.D., Errington J., Rader B., Galiszi A., Galleron N.,

Rantian K.D., Errington J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

Robysshi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Robysshi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

Robysshi Y., Lardinois S., Lauber J., Lazarevic V.,

Ray Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

Ray Medina N., Melllado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

Ray Ray O., Orbil T.M., Porteteile D., Porwollik S., Persecott A.M.,

Ray Ray O., Orbil T.M., Porteteile D., Porwollik S., Staff Park S.,

Ray Sator E., Scholar E., Rocha B., Rapoport G., Sadaie Y.,

Ray Rieger M., Rivolta C., Rocha B., Rapoport G., Sadaie Y.,

Ray Rieger M., Rivolta C., Rocha B., Rapoport G., San M.,

Ray Satoro V., Bohn T.M., Wedler E., Wedler H., Weitzenegger T.,

Ray Anters P., Wilamakoshi A., Tanaka T., Tarkamah H., Takemanu K.,

Takeuchi M., Tamankoshi A., Tanaka T., Tarkamah K., Yasanotti A.,

Ray Anters P., Wilama H.F., Zumstein E., Yoshikawa H., Danchin A.,

Rhe G., Waltiak A., Yasanatoe G. the Gram-positive bacterium Bacillus R.,

Rhylis R., Weller E., Weller E., Weller R.,

Rhylis R., Weller B., Weller E.,

Rhylis R., Weller B., Rapoport G., Weller R.,

Rhylis R., Weller B., Weller R.,

Rhylis R., Weller R., Weller R.,

Rhylis R., Weller R.,

Rhylis R., Weller R.,

Rhylis R., Weller R.,

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"First steps from a two-dimensional protein index towards a response-
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=168;
Kasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
"A 148 kbp sequence of the region between 35 and 47 degree of the
Bacillus subtilis genome.";
Submitted (MAR-1997) to the EMBL/GenBank/DDDJ databases.
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MEDLINE=97443988; PubMed=9298659;
Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,
                                                                                             / Match 3.7%; Score 10; DB 1; Length 281; Local Similarity 100.0%; Pred. No. 0.028; les 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Firmicutes; Bacillales; Bacillaceae; Bacillus.
155 155 BY SIMILARITY.
281 AA; 29350 MW; D50A4CC9167A113E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GS33 BACSU STANDARD; PRT; 285 AA. P80873; P96577; Created)
15-UVL-1998 (Rel. 35, Created)
15-UVL-1998 (Rel. 34, Last sequence update)
General stress protein 39 (GSP39) (EC 1.-.-).
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                                                                                                                                                                                                                                                                15 VALITGGASG 24
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NCBI_TaxID=1423;
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G839 BACSU

D7 G836 BACSU

D7 G8 FEBB-

D6 G8 Bactilu

C8 Bactilu

C9 Bactilu

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Hilbert H., Ubesterhoeft A., Pohl T.M., Weltzenegger T.,
"Analysis of the Bacillus subtilis genome: cloning and nucleotide
sequence of a 62 kb region between 275 degrees (rrnB) and 284 degrees
regulation map for Bacillus subtilis.";
Electrophoresis 18:1451-1463(1997).
-!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
LIMITATION AND OXYGEN LIMITATION.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
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MUBCLINE=98044033; PubMed=9384377;
Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Hypothetical oxidoreductase yuxG (EC 1.-.-.) (ORF2).
YUXG OR YULA.
Bacillus subtilis.
Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.
101 TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
E -> G (IN REF. 3).
P -> K (IN REF. 3).
9BA7EF096B2C9AAE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z99106; CAB12226.1; -.
PIR, D69768, D69768.
Subrilist; BG12052; VdaD.
InterPro; IPRO002198, ADH short.
PRINTS; PRO0060; adh short.
PRINTS; PRO0060; ABN SHORT; 1.
PRINTS; PRO0060; ADH SHORT; 1.
OXIGOSTER; PRO0060; ADH SHORT; 1.
OXIGOSTER; PRO0060; ADH SHORT; 1.
OXIGOSTER; PRO0060; ADH SHORT; 1.
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MEDLINE=97419515; PubMed=9274030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiology 143:2769-2774(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z99106; CAB12226.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 21 E
26 26 P
285 AA; 30951 MW;
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Best Local Similarity 100.0
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P40747;
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NP BIND
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CONFLICT
CONFLICT
SEQUENCE
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Condemine G., Robert-Baudouy J.;
"Analysis of an Erwinia chrysanthemi gene cluster involved in pectin
                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pectobacterium.
               01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-deoxy-b-gluconate 3-dehydrogenase (EC 1.1.1.125) (2-keto-3-
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92114798; PubMed=1766386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 5:2191-2202(1991)
                                                                                                                                       deoxygluconate oxidoreductase)
                                                                                                                                                                                                   Erwinia chrysanthemi
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         degradation.";
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SORD KLEPN
P37079;
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Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Goawa K., Ogiwara A., Oudega B., Park S.H.,
A Noone D., O'Reilly M., Portetelle D., Rosell D., Nakai S., Prescott A.M.,
Parro V., Pohl T.M., Portetelle D., Ropoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha B., Roche B., Rose M., Sadaie Y.,
A Rieger M., Tanakoshi A., Tanaka T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Tarpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
A Yoshida K., Yoshikawa H.F., Zumstein Bacillus
Entits ", "Entits ", "En
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STRAIN=168 / O11085;
MEDLINE=4245722; PubMed=8188684;
MEDLINE=4245722; PubMed=8188684;
Manlon D.W., Ordal G.W.;
"Cloning and characterization of genes encoding methyl-accepting chemotaxis proteins in Bacillus subtilis.";
"J. Biol. Chem. 269:14038-14046(1994).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pfam; PF00596; Aldolase II; 1.
PROSTTE; PS00061; ADH SHORT; 1.
Hypothetical protein; Oxidoreductase; Complete proteome.
ACT_SITE 579 S79 SY STMTIADITY
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100.0%; Pred. No. 0.62;
ive 0; Mismatches
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SubtiList; BG10947; yuxG.
InterPro; IPR002198; ADH short.
InterPro; IPR001303; Aldolase_II_N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=1033-5914 / KAY2026;
MEDLINE=95035038; Pubmed=7947968;
Webnicier U.F., Lengeler J.W.;
"Sequence of the sor-operon for L-sorbose utilization from Klebsiella
-1- CATALYTIC ACTIVITY: 2-deoxy-D-gluconate + NAD(+) = 3-dehydro-2-deoxy-D-gluconate + NADH.
-1- PATHMAY: Pectin degradation.
-1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Enterobacteriaceae, Klebsiella.
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253 AA; 27275 MW; 59E9827DEA471F76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphate dehydrogenase) (Ketosephosphate reductase).
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUT-1996 (Rel. 34, Last annotation update)
Sorbitol-6-phosphate 2-dehydrogenase (EC 1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 8; DB 1;
100.0%; Pred. No. 2.7;
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                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
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InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S17711; S17711.
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                                                                                          (SDR) family.
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253 AA

PRT;

STANDARD;

KDUD ERWCH Q05528;

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428 KVALITGGA 436

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--- CAPALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol + NADH.
                                                MEDLINE=95380679; PubMed=7652212;
Reizer J., Reizer A., Saier M.H. Jr.;
Reizer J., Faciuct A., Saier M.H. Jr.;
Reizer J., Faciuctase (SOCE) and the Glucitol-6-P dehydrogenase (SorD) of the Klebsiella pneumoniae L-sorbose operon belong to the zinc-dependent dehydrogenase family and the short chain alcohol dehydrogenase family, respectively.";
Res. Microbiol. 146:183-184 (1995).
-!- CATALYTIC ACTIVITY: D-sorbitol 6-phosphate + NAD(+) = D-fructose 6-phosphate + NADH.
-!- PATHWAY: SORBITOL METABOLIC PATHWAY.
-!- SUBWINT: Homotetramer (By similarity).
-!- SUBWINT: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
16-OCT-2010 (Rel. 40, Last annotation update)
(Rel. 2, 3-dihydro-2, 3-diol dehydrogenaee) (2,3-dihydro-2,3-dihydroxyphiphenyl dehydrogenaee) (Riphenyl-cis-diol dehydrogenase)
(2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas pseudoalcaligenes.
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
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BY SIMILARITY.
; 44A9C31964384DEC CRC64;
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 pneumoniae KAY2026.";
Biochim. Biophys. Acta 1208:348-351(1994).
                                                                                                                                                                                                                                                                                                                              EMBL, X66059; CAA46856.1; --
PIR, S50186; S50186.

PIRSP, P50162; 1AE1.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PROSTIE; PR00060; SDRFAMILY.
PROSTIE; PR0061; ADH SHORT; 1.
PROSTIE; PR0061; ADH SHORT; 1.
PROSTIE 160 160 BY SIMILARI
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160 160 B
267 AA; 29005 MW;
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                                                                                                                                                                                                              (SDR) family.
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SEQUENCE
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P08694;
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MEDLINE=98318037; PubMed=9655311;
HuelBameyer M., Hecht H.-J., Niefind K., Hofer B., Eltis L.D.,
HuelBameyer M., Schomburg D.;
"Crystal structure of cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase
from a PCB degrader at 2.0-A resolution.";
Protein Sci. 7:1286-1298 (1998).
-!-CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +
NAD(4) = biphenyl-2,3-diol + NADB.
-!-PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) TO
BENZOTC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
-!-SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
-!- PATHWAY: DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) T
BENZOIC ACID AND CHLOROBENZOIC ACIDS; SECOND STEP.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Cis-2,3-dihydrobiphenyl-2,3-diol dehydrogenase (EC 1.3.1.56)
Gis-2,3-dihydroxybiphenyl dehydrogenase) (E.3.3-dihydroxybiphenyl dehydrogenase) (Biphenyl-cis-diol dehydrogenase) (2,3-dihydroxy-4-phenylhexa-4,6-diene dehydrogenase).
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Hofer B., Ellis L.D., Dowling D.N., Timmis K.N.;
"Genetic analysis of a Pseudomonas locus encoding a pathway for
biphenyl/polychloriated biphenyl degradation.";
Gene 130.47-55(1993).
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Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiacee; Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 8; DB 1; Length 275; 100.0%; Pred. No. 2.9; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hastriction TR002198; ADH_short.
Pfam, PF00106; adh_short.
PRINTS; PR00106; aDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
NP_BIND
9 33 NAD (BY SIMILARITY).
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F32A4A870B47E566 CRC64;
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HSSP; P47227; 1BDB.
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ACT_SITE 153 153 B
SEQUENCE 275 AA; 28726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0
Matches 8; Conservative
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                                                                                                               (SDR) family.
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17 LITGGASG 24
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                                                                                                                                                                                                                                                                                                               Similarity
8; Conserva
                                     putida
                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                      (SDR) family.
                                                          NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=292;
                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                GSHR BURCE
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                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
GSHR_BURCE
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      the European Bioinformatics Institute. There are no restrictions on its mode by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                  PRINTS; PRO106; adh short; 1.
PRINTS; PRO106; adh short; 1.
PRINTS; PRO1061; ADH SHORT; 1.
AROSITE; PS00061; ADH SHORT; 1.
Aromatic hydrocarbons catabolism; Oxidoreductase; NAD; 3D-structure. NP BIND 9 33 NAD (BY SIMILARITY).
ACT SITE 155 BY SIMILARITY.
5 STRAND 7 11
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                                                                                                                                                                                                                                                                                                                                                                              Length 277;
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                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 8; DB 1
100.0%; Pred. No. 2.5
1ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              2.9%,
100.0%; Pre-
0;
                                                 PIR; JN0814; JN0814.
PDB; 1BDB; 12-NOV-97.
InterPro; IPR002198; ADH_short.
                                           EMBL; X66122; CAA46909.1; -. PIR; JN0814; JN0814;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                 241
243
251
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                                                                                                                                                                                                                                                                                                                                                           274 :
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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the
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P72220;
16-OCT-2001 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Khan A.A., Wang R.F., Nawaz M.S., Cerniglia C.E.; "Nucleotide sequence of the gene encoding cis-biphenyl dihydrodiol dehydrogenase (bphB) and the expression of an active recombinant Histagged bphB gene product from a PCB degrading bacterium, Pseudomonas putida OUB3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FERS Microbiol. Lett. 154:317-324(1997).
-!- CATALYTIC ACTIVITY: Cis-3-phenylcyclohexa-3,5-diene-1,2-diol +
NAD(+) = biphenyl-2,3-diol + NADH.
-!- PATHWAY DEGRADATION OF BIPHENYLS AND POLYCHLOROBIPHENYLS (PCB) T
BENZOIC ACID AND CHLOROBRAZOIC ACIDS; SECOND STEP.
-!- SUBUNIT: Homotertramer (Probable).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
16-OCT-2001 (Rel. 40, Last annotation update)
(16.2,3.4hydroblabhenyl-2,3.4iol dehydrogenase (EC 1.3.1.56)
(Biphenyl-2,3.4ihydro-2,3.4iol dehydrogenase) (2,3.4ihydro-2,3.4ihydro-2,3.4ihydro-2,3.4ihydro-2,3.4ihydro-2,3.4ihydrogenase) (Biphenyl-cis-diol dehydrogenase)
                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Burkholderiaceae, Burkholderia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send un.

R MSSP; P47227; IBDB.
R HSSP; P47227; IBDB.
R InterPro; IPR00198; ADH short.

DR PRINTS; PR00106; adh short; 1.

DR PRINTS; PR00060; SDRFAMILY.

DR PROSITE; PS00061; ADH SHORT; 1.

DR Aromatic hydrocarbonis catabolism; Oxidoreductase; NAD.

33 NAD (BY SIMILARITY).

155 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 277;
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                                                                                                                                       (2, 3-dihydroxy-4-phenylhexa-4, 6-diene dehydrogenase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glutathione reductase (EC 1.8.1.7) (GR) (GRase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%; Score 8; DB 1;
100.0%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burkholderia cepacia (Pseudomonas cepacia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97457193; PubMed=9311131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=AC1100;
MEDLINE=95266809; PubMed=7538273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Daubaras D.L., Hershberger C.D., Kitano K., Chakrabarty A.M.;
"Sequence analysis of a gene cluster involved in metabolism of 2,4,5-
triculorophenoxyacetic acid by Burkholderia cepacia AC1100.";
Appl. Environ. Microbiol. 61:1279-1289(1995).
-!- CATALYTIC ACTIVITY: 2 glutathione + NADP(+) = glutathione
disulfide + NADPH.
-!- COPACTOR: FAD.
-!- FATHWAY. 2.4,5-trichlorophenoxyacetic acid degradation.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MISCELLARBOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE
OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=272;
MEDLINE=21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 2.9%; Score 8; DB 1; Length 449; Local Similarity 100.0%; Pred. No. 4.4; es 8; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R27A_SCHPO STANDARD; PRT; 136 AA. 014388, 074167; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-FRB-2003 (Rel. 41, Last annotation update) RPL27A OR SPBC685.07C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 HGAKVAIA 43
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
A Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Collins M., Connor R., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornbby T., Howarth S., McDonald S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Sances K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Sharp S.,
RA Retlon J., Simmonds M., Squares R., Squares R., Stavens K.,
RA Mocdward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Meligns I., Vanstreels E., Rieger M., Schaefer M., Mnibert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
R Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
R Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
R Dominguez A., Revuelta J.L., Moceno S., Armstrong J., Foreburg S.L.,
RA Schalber M., Gallardin C., Tallada V.A., Garzon A., Thode G.,
R Dominguez A., Revuelta J.L., McCombie W.R., Paulsen I., Potashkin J.,
R Sphkovski G.V., Ussery D., Barrell B.G., Nurse P.;
R The genome sequence of Schizosaccharomyces pombe.";
R Neure 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"S.pombe ribosomal protein L27 homolog.";
"S.pombe ribosomal protein L27 homolog.";
Submitted (UNN-1998) to the EMBL/Genbank/DDBJ databases.
--- MISCELLANEOUS: THERE ARE TWO GENES FOR L27 IN S.POMBE.
--- SIMILARITY: BELONGS TO THE L27E FAMILY OF RIBOSOWAL PROTEINS.
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Jang Y.J., Yoo H.S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.6%; Score 7; DB 1;
100.0%; Pred. No. 16;
:ive 0; Mismatches
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EMBL; U97385; AAB63877.1; --
EMBL; AB015354; BAA28849.1; --
PIR; T40638; T40638.
PIR; T43374; T43374; GeneDB_SPombe; SPBC685.07c; --
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Best Local Similarity 100..
Log 7; Conservative
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Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
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 Lloyd C.
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                                                                                                                                                                                                                                                                                                                         SUBUNIT: Homodimer; disulfide-linked.
SUBCELLULAR LOCATION: Cytoplasmic.
SUBCELLULAR LOCATION: Cytoplasmic.
CISSUE SPECIFCITY: BODY WALL GLOBIN IS LOCALIZED IN CELLULAR COMPARTMENTS BELONGING TO THE HYPODERMIS, THE DORSAL, VENTRAL AND LATERAL CORDS, THE NETVE RING, AND BODY WALL MUSCLE.
PTM: THE N-TERMINUS IS BLOCKED.
SIMILARITY: Belongs to the globin family.
                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1906 (Rel. 34, Last annotation update)
Myoglobin (Globin, body wall isoform).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Elukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                             TISSUE-Body wall muscle;
MEDLINE=95074010; PubMed=7982924;
Blaxter M.L., Vanfleteren J.R., Xia J., Moens L.;
Blaxter M.L., Vanfleteren J.R., Xia J., Moens L.;
J. Biol. Chem. 269:30181-30186(1994).
-I- FUNCTION: HIGH OXYGEN AFFINITY. PROBABLY SUPPLIES OXYGEN NEEDED FOR MUSCLE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 15.4 kDa protein Cl6C10.11 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.6%; Score 7; DB 1; Length 153;
100.0%; Pred. No. 18;
ive 0; Mismatches 0; Indels
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Heme; Oxygen transport; Transport.
Heme; Oxygen transport; Transport.
Heme; Oxygen transport; Transport
Heme; Oxygen transport; Transport
(BY SIMILARITY).
                             153 AA.
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                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P28316; 1ASH.
InterPro; IPR000971; Globin.
Pfam; PF00042; globin; 1.
PROSITE; PS01033; GLOBIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U17337; AAA64695.1; -.
PIR; A55139; A55139.
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Best Local Similarity 100.
                           STANDARD;
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                                                                                                                                                                    NCBI_TaxID=6253;
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YQSB_CAEEL
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AC Q09254;
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PIR, T19332; T19332.
Wormbep; C16C10.11; DUP657.
InterPro; IPR007017; DUP657.
Pfam; PF04933; DUF657; 1.
Hypothetical protein.
SEQUENCE 154 AA; 15388 MW; 5F5C618B637D2683 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               2.6%; Score 7; DB 1;
100.0%; Pred. No. 18;
tive 0; Mismatches
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Q98pps rhizobium m
Q98d94 brucella me
Q84d9 brucella me
Q84d9 brucella me
Q84d9 brucella me
Q84d9 brucella me
Q94c9 arabidopsis
Q81c3 brashidopsis
Q81c4 oryza sativ
Q81c5 brucella su
Q80c9 rhizobium l
Q86c97 oceanobacil
Q86c97 ceanobacil
Q87d10 arabidopsis
Q91f0 sphingopyxi
Q84f0 brucella me
Q95c00 arabidopsis
Q91d1 oryza sativ
Q8f1d1 oryza sativ
        Q8lid3 oryza sativ
Q8fv38 brucella su
Q8kwt4 bacillus su
Q8kws9 bacillus am
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Q97ua4 sulfolobus
Q8khi5 pectobacter
Q9s9w2 arabidopsis
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0928s3 rhizobium m
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095tl streptomyce
09fbtl streptomyce
28wzx3 neurospora
QBWZX3
QBRIJD3
QBRIJD3
QBRIVT4
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094k17 forsythia i
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092x17 arabidopsis
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08164 oryza sativ
08164 ipomoea tri
0918bd7 ipomoea tri
0918bd8 ipomoea tri
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0918bd8 ipomoea tri
08165 ipomoea tri
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(c) 1993 - 2003 Compugen Ltd.
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163 7 2.6 250 2 Q8GDE6 164 7 2.6 251 2 Q9F7E0 165 7 2.6 251 5 Q9V671 167 7 2.6 251 10 Q40133 167 7 2.6 251 16 Q8PE31	7 2.6 252 4 7 2.6 252 16 7 2.6 252 17	7 2.6 253 16 7 2.6 254 16 7 2.6 255 16	7 2.6 255 16 7 2.6 255 16 7 2.6 257 16	7 2.6 257 16 7 2.6 258 16 7 2.6 258 16	7 2.6 258 16 7 2.6 259 10 7 2.6 259 16	7 2.6 260 16	7 2.6 261 16 7 2.6 261 16 7 2.6 261 16	7 2.6 261 16	7 2.6 264 16 7 2.6 264 16 7 2.6 267 16	7 2.6 269 2	7 2.6 274 16	7 2.6 281 17	7 2.6 282 13 7 2.6 286 10 7 2.6 286 16	7 2.6 287 10 7 2.6 289 16	7 2.6 297 15 7 2.6 298 10 7 2.6 300 16	7 2.6 306 10	7 2.6 308 16 7 2.6 315 6	7 2.6 316 10	7 2.6 317 5 7 2.6 323 16	7 2.6 328 16 7 2.6 329 2	7 2.6 331 16	7 2.6 339 B	7 2.6 340 17 7 2.6 346 2 7 2.6 346 5	7 2.6 353 5 7 2.6 353 16	7 2.6 355 16 7 2.6 357 5	7 2.6 362 16	7 2.6 366 16 7 2.6 366 16	•
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8 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHC 67
                                                                                                                           12 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHC 71
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MEDLINE=95004656; PubMed=720706;
MEDLINE=95004656; PubMed=720706;
MA cis-acting element and a trans-acting factor involved in the wound-induced expression of a horseradish peroxidase gene.";
plant J. 6:87-97(1994).
-!- SIMILARITY; BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
80-MR-2003 (TrEMBLrel. 23, Last annotation update)
80-MY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TFHP-1 protein.
Nicotiana tabacum (Common tobacco).
Nicotiana tabacum (Common tobacco).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                           Ouery Match 6.2%; Score 17; DB 10; Length 234; Best Local Similarity 100.0%; Pred. No. 1.4e-09; Matches 17; Conservative 0; Mismatches 0; Indels
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase.
SEQUENCE 234 AA; 25078 MW; F10BD4E0FF97940A CRC64;
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MEDLINE-96145513; PubMed-8555446;
MEDERS K., Moenke G., Badur R., Sonnewald U.;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDR) PAMILY.
EMBL, D29976; BAA06241.1;
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 RLEGKVALITGGASGIG 26
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    110; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Q40590;
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    Matches
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                                                                                                         091fp2 arabidopsis
084674 paramecium
08x46 atraptomyce
09xk6 atraptomyce
09xk6 atraptomyce
09xk9 patentella
09clg8 patentella
09clg8 patentella
09c69 lactococcus
09gh4 xanthomonas
00f60 saccharcmyc
00388 saccharcmyc
00388 saccharcmyc
00388 saccharcmyc
00388 saccharcmyc
0039d6 streptococcus
099d6 streptococcus
099d6 streptococcus
099d6 streptococcus
08c0 salmonella
08c0 salmonella
08c16 secherichia
08c16 cocanobacia
08c16 secherichia
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094KL7
01-DEC-2001 (TERMELrel. 19, Created)
01-DEC-2001 (TERMELrel. 19, Last sequence update)
01-DEC-2003 (TERMELrel. 23, Last annotation update)
51-DEC-2003 (TERMELrel. 23, Last annotation update)
52-DEC-2003 (TERMELrel. 23, Last annotation update)
53-DEC-2003 (TERMELrel. 23, Last annotation update)
54-DEC-2003 (TERMELrel. 23, Last annotation update)
55-DEC-2003 (TERMELrel. 23, Last annotation update)
65-DEC-2003 (TERMELRel. 23, Last annotation update)
67-DEC-2003 (TERMELRel. 23, Last annotation update)
68-DEC-2003 (TERMELRel. 23, Last annotation update)
68-DEC-2003 (TERMELRel. 23, Last annotation update)
69-DEC-2003 (TERMELRel. 23, Last annotation upd
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Modification and the state of 
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                                                                                                                                                     Q84674
Q8XU43
Q9EXK6
Q9CLG8
Q8CKG9
Q9CCG9
Q9CCG9
Q9CCG9
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Q8ZFTS
Q8FJU6
Q8ETD2
Q8EAWS
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Q8NZN2
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Q9RZ49
Q99YD6
Q97Q07
Q8ZQV6
Q8ZBD9
Q8X9C8
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Q8M0C9
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InterPro; IPR02198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SBRPAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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Best Local Similarity
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01-DD T 01-DD
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11 LEGKVALITGGASGIG 26
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NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Putative alcohol dehydrogenase.
F4C21.6 OR AT4003140.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
                    photoassimilate responding genes: isolation of cDNAs encoding a new class of pathogenesis related proteins "; Plant Mol. Biol. 29:1027-1038(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM.", Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
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Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,
McCombie W.R.;
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"A simplified procedure for the subtractive cDNA cloning of
                                                                                                                                                                                                                                                                                                                                                                                                            Length 284;
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.2%; Score 17; DB 10; Length 28
Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 17; Conservative 0; Mismatches 0; Indels
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                       284 AA; 29819 MW; BD884E9013FB63E9 CRC64;
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                           EMBL; AJ223179; CAA11154.1; -... EMBL; AJ223177; CAA11153.1; -... HSSP; P19992; IHDC. InterPro; IPR002198; ADH short. Ffan; PF00106; adh short; IPRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT; 1...
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Pfam; PF00106; adh short; 1.
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PROSITE; PS00061; ADH_SHORT; 1.
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                                                                                                                             (SDR) FAMILY.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 23, Last annotation update)
Alcohol dehydrogenase-like protein (At3g26770/MDJ14_21).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Angnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Arabidopsis cDNA clones.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodersa C.S., Palla C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                              0941E4;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                         306 AA
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                                                                                                                                                                                                                                                         AT3926770/MDJ14_21.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AY052216; AAK97686.1; -.
InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
18 LEGKVALITGGASGIG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 LEGKVALITGGASG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 LEGKVALITGGASG 54
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                                                                                                                                       PRELIMINARY;
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Created) Last sequence update) Last annotation update) 274 AA.

PRT;

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Phaseolus lunatus (Lima bean) (Phaseolus limensis).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
NCBI_TaxID=3884;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

Michidel J., Atimura G., Ozawa R., Muroi A., Takabayashi J.,
Nishioka T.,
"Phaseolus T.,
"Phaseolus Junatus",
Submitted (JUN-202) to the EMBL/GenBank/DDBJ databases.
Shall, abacs3872.1; -.
SEQUENCE 274 AA; 28862 MW; DEC858BDB324877F CRC64;
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Local Similarity 100.0%; Pred. No. 3.5e-05;
es 13; Conservative 0; Mismatches 0; Indels
                                                                                                                  01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
Alcohol dehydroge.
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                                                                  PRELIMINARY;
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               RESULT 8
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                                                                                            Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
Chang C.H., Dale J.M., Deny J.M., Hayashizari Y.
A chan W.M., Chang C.H., Dale J.M., Deng J.M., Hayashizari Y.
Hauan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Palm C.J., Quach H.L., Sakuran T., Satou M., Seki M.
Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
R. Santakidopsis or Pre Choriumi M., Wallender E.K., Wong C., Wu H.C.,
B. Shilaharia S., Shinozaki K., Davis R.W., Theologis A.,
E.Ker J.R.,
Shilaharia BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
C. (SDR) PAMILY. BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
C. (SDR) PAMILY.
EMBL, AND1689; BAB01223.1; -.
REMEL, AND1689; BAB0123.1; -.
REMEL, AND1689; ADH.Short.
REMEL, PRO92196; adh short.
                                                                                                                                                                                                                                           H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 22, Last sequence update)
CPRD12 protein.
Bugna unguiculata (Cowpea).
Bugna unguiculata (Cowpea).
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Rosidae; MCBL TaxID=3917;
NCBI_TAXID=3917;
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Undi S., Yamaguchi.-Shinozaki K., Urao T., Shinozaki K.;

"Characterization of two CDNAs for novel drought-inducible genes in the highly drought-tolerant cowpea.";

J. Plant Res. 109:415-42(1996).

-!- 'AMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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100.0%; Pred. No. 3.4e-05;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8E87A72D081266EB CRC64;
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SEOUENCE 267 AA; 28484 MW; 8C4A48A2E9F41B64 CRC64;
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BMBL, D88121; BAA13541.1; -.

HSSP, P19992; 1HDC.

InterPro; IPR002199; ADH short.

Pfam; PF00106; adh short; 1.

PRINTS; PR00106; SDRPAMILY.
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SEQUENCE 306 AA; 31783 MW;
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   clones.";
DNA Res. 7:131-135(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 AVELGQFGIRVNC 190
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es 14; Conserv
                                                                            SEQUENCE FROM N.A.
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les 13; Conserv
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Best Local S
Matches 13
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PRINTS;
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P93697;
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Matches
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Length 274;

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SEQUENCE FROM N.A.

STRAIN=CV. Nipponbare;

STRAIN=CV. Nipponbare;

Sasaki T., Matsumoto T., Katayose Y.;

"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC

clone:P0453E03..;

slubmitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

-! STMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

EMBL, AP003425; BAC10093.1;

EMBL, AP003425; BAC22441.1;

Gramene; QBLID4; -.
                                                                                                                                                                                                                                                                                                                                                                                                            0.1-0cr.-2002 (TrEMBLrel. 22, Created)
0.1-0cr.-2002 (TrEMBLrel. 22, Last sequence update)
0.1-0cr.-2003 (TrEMBLrel. 23, Last sequence update)
0.1-343_D04.14 protein (P0453E03.33 protein).
0.01343_D04.14 protein (P0453E03.33 protein).
0.01343_D04.14 or P0453E03.33.
0.01343_D04.14 or P0453E03.33.
0.01343_D04.14 or P0453E03.33.
0.01343_D04.14 or P0453E03.33.
0.001343_D04.14 or P045
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STRANTE-CV. NIPPODNDATE;
SABAKI T., Mateumoto T., Yamamoto K.;
"Oryza attiva nipponbare(GA3) genomic DNA, chromosome 7,
clone:041343 D04".
Submitted (JÜL-201) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 AA; 34337 MW; 3DB5EC4726D98AA2 CRC64;
                                                                                                                                                                                                                                                                                                             PRT; 321 AA
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178 AVELGOFGIRVNC 190
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
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SEQUENCE 321
                                                                                                                                                                        RESULT 9
09L104
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09L104
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Matches

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"Characterization of promoter region of the SSP gene from Ipomoea trifida regulates stigma-specific expression."; Submitted (AUG-2001) to the EWBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                          277 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 AA.
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                                                                             InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SDR) FAMILY.
EMBL; AF072448; AAC35341.1; -.
HSSP; P19992; IHDC.
                                                                                                                                                                                                                                                                                                                        89 YGKLDIMFSNAG 100
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                             12; Conservative
                                                                                                                                                                                                                                                                                          86 YGKLDIMFSNAG 97
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                 (SDR) FAMILY.
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                                                                                                                                                                              Oxidoreductase
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SEQUENCE 277
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09SBD8
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Kowyama Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
Kondo K., Norioka S.;

Kondo K., Norioka S.;

"S-locus specific stigma protein (SSP) from sporophytic self-
incompatibility plant, Ipomoea trifida, is a member of short-chain
alcohol dehydrogenase family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-H45-3;
Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Kowyama Y.;
Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Kowyama Y.;
"Characterization of promoter region of the SSP gene from Ipomoea
trifida regulates stigma-specific expression.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
   Gaps
                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, lamiids, Solanales, Convolvulaceae, Ipomoea.
VCBI_TaxID=35884,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein).
SSP OR SSP10.
Ipomoea trifida.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 160;
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   Indels
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Short-chain alcohol dehydrogenase (S-locus linked stigma
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160 AA; 16817 MW; BAEBFB2727F12684 CRC64;
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01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
S-locus linked stigma protein 1 (Fragment).
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                                                                                                                                              160 AA
 Mismatches
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                               235 AALYLASDEAKYV 247
                                                              287 AALYLASDEAKYV 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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                                                                                                                                              PRELIMINARY;
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Best Local Similarity
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                                                                                                                                                                                                                                                          Ipomoea trifida.
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SEQUENCE
                                                                                                                                                             Q8S9B7;
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RESULT 10
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RESULT 11 Q9SBD7

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KOWYAMA Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,

Kondo K., Norioka S.;

Kondo K., Norioka S.;

"S-locus specific stigma protein (SSP) from sporophytic self-
incompatibility plant, Ipomoea trifida, is a member of short-chain
alcohol dehydrogenase family.",

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                      Gaps
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, lamiids; Solanales; Convolvulaceae; Ipomoea.
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                                                            4.4%; Score 12; DB 10; Length 277;
100.0%; Pred. No. 0.00043;
tive 0; Mismatches 0; Indels
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277 AA; 29257 MW; A0CDB434B31C666D CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
101-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Short-chain alcohol dehydrogenase.
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RESULT 15
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                                                                                                                                                                                                                               Kowyama Y., Kadora N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T.,
Kondo K., Norioka S.;
"S-locus specific stigma protein (SSP) from sporophytic self-
"S-locus specific stigma protein (SSP) from sporophytic self-
incompatibility plant, Ipomoea trifida, is a member of short-chain
alcohol dehydrogenase family.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
[SNP FAMILY. BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
EMBL, APO7450; AAC13343.1; -.
HSSP, P19922; LHDC.
INTEPPO, PIPRO2198; ADH_short.
PRINTS, PRO0106; adh_short.
PRINTS, PRO0106; adh_short.
PRINTS, PRO0106; SDRFAMILY.
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SEQUENCE FROM N.A.

Kakeda K., Tsuchiya T., Ishimizu T.,

Kondo K., Norioka S.;

"S-locus specific stigma protein (SSP) from sporophytic self-
incompatibility plant, Ipomea trifida, is a member of short-chain
alcohol dehydrogense family.";

Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

(SDR) FAMILY.
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Ipomoea trifida.
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Convolvulaceae; Ipomoea.
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100.0%; Pred. No. 0.00044;
ive 0; Mismatches 0; Indels
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4.4%; Score 12; DB 10; Length 28.
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 12; Conservative 0; Mismatches 0; Indels
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HSSP; P19992; THDC.
InterPro; PR002198; ADH short.
Pfam; PF00106; adh_short.
PRINTS; PR00080; SDRPAMILY.
Oxidoreductase.
SEQUENCE 284 AA; 29823 MW; 4C04A888178C0633 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2003 (TrEMBLrel. 23, Last annotation update)
Short-chain alcohol dehydrogenase.
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Best Local Similarity 100.
Matches 12; Conservative
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89 YGKLDIMFSNAG 100

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STRAIN=SU-1;
MEDLINE=2050789; PubMed=11055914;
Chang P.K., Yu J., Ehrlich K.C., Boue S.M., Montalbano B.G.,
Bhatnagar D., Cleveland T.B.;
Hadha in Aspergillus parasiticus Is Involved in Conversion of 5'-
Hydroxyaverantin to Averufin.,
Appl. Environ. Microbiol. 66:4715-4719(2000).
-1-SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                    Aspergillus parasiticus.

Bukaryota, Fungi, Ascomycota, Pezizomycotina, Eurotiomycetes;

Burotiales, Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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4.0%; Score 11; DB 3; Length 278
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 11; Conservative 0; Mismatches 0; Indels
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                       01-JUJ-1997 (TrEMBLrel. 04, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Short-chain alcohol dehydrogenase.
278 AA.
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PRT;
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InterPro: IRR002198; AbH short.
Pfam, PF00106; adh short; I.
PROSITE; PS00061; ADH_SHORT; I.
PRELIMINARY;
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SEQUENCE 278
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Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan; matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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AAG09588
ABB92500
AAY77928
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AAG38248
ABB48207
AAY34891
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ABB92823
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ABB92448
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AAG31795
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AAY44578
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 Forsythia intermedia
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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Compugen Ltd.
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                GenCore version (c) 1993 - 2003
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Gapop 10.0 , Gapext 0.5
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Score

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Kylitol dehydrogen Listeria monocytog Levodione reductas

guboxydans DSM

Chlamydia pneumoni

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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway.

The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 KDa, an isoelectric point of 5.9-6.85, and require corrected are used for the secoisolariciresinol dehydrogenase in plants or to alter lignan, accids are used for the recombinant expression of the enzymes.

It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan, bosynthesis. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase or proteins and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids can be utilized to: elevate or otherwise concerns and nucleic acids and fruits and to food items incorporating material vegetables, grains and fruits and to food items incorporating material vegetables, grains and fruits and to food items incorporating material avariety of purposes, for example as neutriceuticals and dietary auriety of purposes, for example (-) trachogenin which possesses antiviral approximant supply of properties, and (-)-podophyllotoxin.
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New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 100.0%; Score 1393; DB 21; Length 273; Local Similarity 100.0%; Pred. No. 2.2e-130; Los 273; Conservative 0; Mismatches 0; Indels 0;
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                                                                       Claim 8; Page 46-47; 66pp; English.
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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway.

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                                                                                                                        (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                              Lewis NG;
                                                                                                                                                                                                                                                                                                                              Example 2; Page 61-63; 66pp; English.
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N-PSDB; AAZ45743.
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04-NOV-1999
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186 QFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLAS 245
                                                                                                                                                                                     AAY54416 standard; Protein; 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 VIGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 VIGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLGLTRNLAVELG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QVLTAIARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFGIRVNCLSPFGLPTALGKKFSGIKOVEEFENVINFAGNLKGPKFNVEDVANALYLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 QLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
                                                                              Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan, matairesinol, health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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Pred. No. 1.8e-127;
1; Mismatches 4; Indels 0;
                                      Secoisolariciresinol dehydrogenase protein clone SMDEHY321.
                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON STATE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Lewis NG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 49-50; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Costa MA, Davin LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97.98;
                                                                                                                                                                                                                                                                                                                                                  98US-0082977
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  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        267; Conservative
                                                                                                                                                                                 Forsythia intermedia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-126356/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ45731
                                                                                                                                                                                                                         WO9955846-A1.
                                                                                                                                                                                                                                                                                                          23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                  24-APR-1998;
                                                                                                                                                                                                                                                                 04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                Xia Z,
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The secoisolariciteshing a secondariant cannot deploy be protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolaricireshinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolaricireshinol dehydrogenase mucleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolaricireshinol dehydrogenase in plants or to alter lignan biosynthesis. The enzyme is used for production of the pharmacologically active lignan, mataireshinol. The secoisolaricireshinol dehydrogenase proteins and mucleic acids can be utilized to: elevate or otherwise proteins and mucleic acids can be utilized to: elevate or otherwise cortive as encerolactone and enterodiol, in plant species, including phytosetrogeness of the relevance of health-protecting lignans, including phytosetrogenes and fruits and to food items incorporating material derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, and (-)-podophyllotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 QLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway; lignan; matairesinol; health-protecting lignan; phytoestrogen; enterolactone; enterodiol; neutriceutical; dietary supplement; (-)-trachelogenin; antiviral; (-)-podophyllotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secoisolariciresinol dehydrogenase protein clone SMDEHY631.
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ilarity 88.2%; Pred. No. 2.1e-114;
Conservative 14; Mismatches 18;
DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS
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                                                                                                                                                                                                                                                                                  임
                                                                                        The invention relates to a method for increasing the guaiacyl (G)-lignan content in seeds of a monocotyledon plant, comprising selecting at least come protein or enzyme integral to the pathway leading to eliginal formation, stably transforming a monocotyledon plant with chimeric gene (GG) constructs having a seed-specific transcriptional regulatory region operably linked to a mucleic acid sequence encoding the enzyme method of the invention is useful for stably transforming a monocotyledonous plant (e.g. rice) with GG constructs resulting in increased expression of the genes encoded by GG constructs. The G-lignan enriched seed composition is useful as a food additive. This sequence represents the secoisolariciresinol dehydrogenase protein relating to the invention.
                                                                124
                                                                                                                                          OFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLAS 241
                                        STYIHCDVINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVN 121
              64
                                                                                                                                                                                                                                                                                                                                                                                        Guaiacyl (G)-lignan, monocotyledon plant; rice; food additive,
seed-specific transcriptional regulatory region; dehydrogenase; enzyme.
                                                        STYIHCDVINEDGUKNAVDNIVSTYGKLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Increasing gualacyl-lignan content in monocotyledon plants, by transforming plant with chimeric gene construct having seed-specific transcriptional regulator linked to gene encoding protein involved in G-lignan formation
DEAQYVSGQNLFIDGGFSVCNSAIKLFQYPDS 276
                                                                                                                                                                                             DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS 273
                                                                                                                                                                                                                                                                                                                                                                  Secoisolariciresinol dehydrogenase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNIW ) UNIV WASHINGTON STATE RES FOUND. (PHYT-) APPLIED PHYTOLOGICS INC.
                                                                                                                                                                                                                                                                                     AAO21494 standard; Protein; 276 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-425767/45.
N-PSDB; AAL38432.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                        15-AUG-2002
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                                                                                                                   125
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                                                                                                                                                                                                                                                                                                               AA021494;
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65 STYIHCDVINEDGVKNAVDNIVSTYGKLDIMFNNAGISDPYKPRVIDNEKADFERVLSVN 124
                                                                                                                                                                                                                                                                                      STYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVN 121
                                                                                                                                                                                               122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTWGGGSSHAYCGSKHAVLALTRNLAVELG 181
                                                                   61
                                                                                               64
                                                                                                                                                                                                                    182 QFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLAS
                                                                                                 5 QLRTAFARRLEGKVALITGGASGVGEVTAKLFSQHGAKVAIADVQDELGHSVVEAIGLSN
                                                                 2 OLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kba, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase
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Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secoisolariciresinol dehydrogenase protein clone SMDEHY431.
                                Indels
Query Match 88.5%; Score 1233; DB 23;
Best Local Similarity 88.2%; Pred. No. 2.1e-114;
Matches 240; Conservative 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                       DEAQYVSGQNLFIDGGFSVCNSAIKLFQYPDS 276
                                                                                                                                                                                                                                                                                                                                    DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY54414 standard; Protein; 273 AA.
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N-PSDB; AAZ45732.
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                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                           MQLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLRTAIARRLEGKVALITGGASGVGEVTAKLFSQHGAKVAIADVQDELGHSVVEAIGPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSTYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVTGVFLCMKHAARVMI PARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GOFGIRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLA
nucleic acids are used for the recombinant expression of the enzymes
                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secoisolariciresinol dehydrogenase; lignan biosynthetic pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lignan, matairesinol, health-protecting lignan, phytoestrogen, enterolactone, enterodiol, neutriceutical, dietary supplement, (-)-trachelogenin, antiviral; (-)-podophyllotoxin.
                                                                                                                                                                                                                                                                                                                      87.8%; Score 1223; DB 21; Length 273;
86.8%; Pred. No. 2e-113;
iive 15; Mismatches 21; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secoisolariciresinol dehydrogenase protein clone SMDEHY511.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDEAQYVSGQNLFIDGGFSVCNSAIKMFQYPDS
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                                                                                                                                                                                                                                       properties, for example (-)-trachelo
properties, and (-)-podophyllotoxin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0082977
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.8°
Matches 237; Conservative
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                                                                                                                                                                                                                                                                                        273 AA;
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                                                                                                                                                                                                                                                                                        Sequence
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The present sequence represents a secoisolariciresinol dehydrogenase protein. The enzyme is involved in the lignan biosynthetic pathway. The secoisolariciresinol dehydrogenase proteins have a molecular weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require weight of 27-31 kDa, an isoelectric point of 5.9-6.85, and require NAD or NADP as a cofactor. The secoisolariciresinol dehydrogenase concleic acids are used for the recombinant expression of the enzymes. It is also used to obtain expression or enhanced expression of secoisolariciresinol dehydrogenase in plants or to alter lignan active lignan. The enzyme is used for production of the pharmacologically active lignan, matairesinol. The secoisolariciresinol dehydrogenase cortive lignan, matairesinol. The secoisolariciresinol dehydrogenase cortive lignan, matairesinol. The secoisolariciresinol dehydrogenase conterins and mucleic acids can be utilized to: elevate or otherwise such as enterolactone and enterocioli, in plant species, including phytoestrogens such as enterolactone and enterocioli, in plant species, including material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIXIHCDVTNEDDVKNAVDNTVSTYGKLDIMFNNAGIADPNKPRIVDNEKADFERVLSVN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLAS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                             derived from such genetically altered plants; genetically alter plant species to provide an abundant, natural supply of lignans useful for a variety of purposes, for example as neutriceuticals and dietary supplements; to genetically alter living organisms to produce an abundant supply of optically pure lignans having desirable biological properties, for example (-)-trachelogenin which possesses antiviral properties, and (-)-podophyllotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 QLRTAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 QVLTAITRRLEGKVALITGGASGIGEFTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                           New nucleic acid molecule encoding an enzyme involved in lignan biosynthetic pathway, useful for producing large amounts of lignans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.4%; Score 1175; DB 21;
83.5%; Pred. No. 1.3e-108;
tive 20; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herbicidally active polypeptide SEQ ID NO 540.
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                                                                                                                          Claim 8; Page 54-55; 66pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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WPI; 2000-126356/11.
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Matches 227; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277 AA;
                   N-PSDB; AAZ45733
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQF 183
                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                               8 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI--GTSNST-- 63
                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridiation sasay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                        Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences.from non-plant organisms -
                                                                                                                                                                                                                                                                                                                     Query Match

Query Match

47.3%; Score 658.5; DB 23; Length 285;
Best Local Similarity 50.9%; Pred. No. 4.4e-57;

Matches 139; Conservative 43; Mismatches 78; Indels 13; Gaps
                                                                                                                                                                           Claim 5; SEQ ID NO 540; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 29625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              237 LYLASDEAKYVSGHNLFIDGGFSVCNSVIKVFQ 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||||:::|:|| || || ||||:
253 LFLASDDSRYISGDNLMIDGGFTCTNHSFKVFR 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG25524 standard; Protein; 285 AA.
                                        28-AUG-2001; 2001WO-EP09892
                    28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                Tietjen K, Weidler M;
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                                                                                                     WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                     Sequence 285 AA;
                                                             (FARB ) BAYER AG.
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RR 05-MAR-1999; 99US-0123180.

RR 23-MAR-1999; 99US-0123548.

RR 23-MAR-1999; 99US-0125788.

RR 06-APR-1999; 99US-0126785.

RR 10-APR-1999; 99US-0128244.

RR 10-APR-1999; 99US-01310491.

RR 23-APR-1999; 99US-01310491.

RR 23-APR-1999; 99US-01310491.

RR 23-APR-1999; 99US-01310491.

RR 23-APR-1999; 99US-0131449.

RR 23-APR-1999; 99US-0131449.

RR 23-APR-1999; 99US-0131449.

RR 24-MAY-1999; 99US-01314218.

RR 14-MAY-1999; 99US-01314218.

RR 14-MAY-1999; 99US-01314218.

RR 14-MAY-1999; 99US-01316221.

RR 12-MAY-1999; 99US-01316221.

RR 11-MAY-1999; 99US-01316222.

RR 11-MAY-1999; 99US-0131622.

RR 11-MAY-1999; 99US-0131622.

RR 11-MAY-1999; 99US-01316
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64 YIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVT 123
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47.0%; Score 654.5; DB 21; Length
Best Local Similarity 50.9%; Pred. No. 1.1e-56;
Matches 139; Conservative 42; Mismatches 79; Indels
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                   990S-0155486
990S-0155486
990S-0156559
990S-0156569
990S-0157753
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                     23.SEP-1999;
24.SEP-1999;
29.SEP-1999;
29.SEP-1999;
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06-0CT-1999;
07-0CT-1999;
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99US-0151930.
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99US-0154018.
99US-0154039.
99US-0154779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SVNVTGVFLCMKHAARVMIP-ARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 VELGQFGIRVNCLSPFGLPTAL----GKKFSG--IKNE--EEFENVINFAGNLKGPKFNV 229
                                                                                                                                                                                                                                                                The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the B-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 20101
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Herbicidally active polypeptide SEQ ID NO 1835.
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nes 131; Conservative
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188 NCLSPFGLPTA-----LGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASD 242
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Matches 126; Conservative
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22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
12-0CT-1999;
12-0CT-1999;
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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        14 - JWN - 1999
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        16 - JWN - 1999
        90US-0139452

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        17 - JWN - 1999
        90US-0139452

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        18 - JWN - 1999
        90US-0139452

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        28 - JWN - 1999
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        29 - JWN - 1999
        90US-0139452

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        23 - JWN - 1999
        90US-0139452

        PR
        23 - JWN - 1999
        90US-0140353

        PR
        23 - JWN - 1999
        90US-0141234

        PR
        24 - JWN - 1999
        90US-01412320
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135-014831 135-014834 135-014868 135-014936 135-014936 135-014942 135-014942 135-014993 135-014993 135-014993	105 - 015 088	US-0155294 US-0155291 US-01553310 US-01553310 US-01553310 US-0160741 US-0160741 US-0160740 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0160910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910 US-0161910
AUG-1999; 9	AUG-19999;	
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Query Match
42.9%; Score 597.5; DB 21; Length 283;
Best Local Similarity 47.0%; Pred. No. 5.3e-51;
Matches 126; Conservative 45; Mismatches 86; Indels 11; Gaps

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VTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                                                                    CLSPFGLPTA----LGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPMPKRLDGKVAIVTGGARGIGEAIVRLFAKHGARVVIADIDDAAGEALASALGPQVS-F 105
              Tasselseed 2; Ts2; maize; H2 clone; rice; floral tissue; male; female;
bacterial hydroxysteroid dehydrogenase; sexual development; flower.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the tasselseed 2 (Ts2) protein derived from maize. This sequence is encoded by the H2 clone. The Ts2 protein in maize is very similar to Ts2 protein found in rice, and both these sequences show considerable homology to bacterial hydroxysteroid dehydrogenases. Ts2 has a mol. wt. of 35 kD and a predicted pI of 6.7. The Ts2 coding sequence and its promoter, may be used to control sexual development of floral tissue and to provide exclusively male
                                                    MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 TAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tasselseed 2 gene and promoter and expression systems for transforming plants - for controlling sexual development either predominantly male or female flowers, to simplify cross-breeding and production of hybrid seeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IndelB
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42.2%; Pred. No. 5.4e
:ive 50; Mismatches
                                                                                                                                                                             AKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
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                                                                                                                                                                                                                                                           AAW06488 standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 6; 44pp; English.
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N-PSDB; AAT45060.
                                                                                                                                                                                                                                                                                                                                         Maize Ts2 sequence.
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Matches 122; Conserv
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         VINEDGVKONAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                         IKHAARVMIPRNSGSIICAGSVTGMMGGLAQHTYSVSKSAVIGIVRSTASELCKHRIRVN 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKHAARVMI PARSGNI I STASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN
                                                                                                                 CLSPFGLPTA----LGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLASDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequenc from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23; Length 283;
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47.0%; Pred. No. 5.3e-51;
ive 45; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                   Herbicidally active polypeptide SEQ ID NO 2034.
                                                                                                                                                                                       AKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
                                                                                                                                                                                                                                                                                                                                                                               Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                     ABB92823 standard; Protein; 283
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                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tietjen K, Weidler M;
                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER AG
                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200210210-A2.
                                                                                                                                                                                                                                                                                                                           31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-2002
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28677, A 4825, Ap 30474, A 26759, A 2, Appli 2, Appli

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence

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Sequence Sequence Sequence

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Perfect score:

Sequence:

protein

Run on

Scoring table:

Searched:

Minimum DB Maximum DB

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65 IHCDVTNEDGVKNAVDNTVSTY-GKLDIMFSNAGI---SDPNRPRIIDNEKADFERVLSV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08440856A

Patent No. 5750873

GENERAL INFORMATION:
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 2000 FENNSYLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem PC COMPUTER:
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: LS-MAY-1995
CLASSIFICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFRENCE/DOCKET NUMBER: 36,217
RELEPENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELEPENCE. (202) 887-0763
                          US-09-134-001C-4825
US-09-252-991A-26759
US-09-252-991A-26759
US-09-272-810A-2
US-09-328-132-5703
US-09-328-132-5703
US-08-822-32-8
US-08-846-109-8
US-08-594-8088-7
US-09-252-991A-28482
US-09-328-322-7773
US-09-328-322-7773
US-09-338-322-7773
US-09-634-955B-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-28291
                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-634-955B-17
US-09-634-955B-20
US-09-328-352-5565
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.28
Matches 122; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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US-08-440-856A-3
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Sequence 4, Appli
Sequence 8, Appli
Sequence 24032, A
Sequence 5742, Ap
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
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1 MQLRTAFARRLEGKVALITG......IDGGFSVCNSVIKVFQYPDS
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/cgn2_6/ptcdata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptcdata/2/iaa/PCTUS_COMB.pep:*
                                 GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd
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US-08-440-856A-4

US-08-440-856A-8

US-09-252-991A-24032

US-09-328-352-5742

US-09-328-352-5742

US-09-504-314-14

US-09-504-314-14

US-09-198-452A-309

US-09-198-6

US-09-198-6

US-09-198-6

US-09-198-6

US-09-198-6

US-09-198-6

US-09-101-29

US-09-101-29

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US-09-101-29

US-09-101-25

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US-08-562-114B-13
US-08-729-594A-13
US-08-937-993-13
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match Length
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Result

349.5 341.5 341.5 341.5 341.5 331.5 324.5 323.3

320 318.5 317.5 317.5 317.5 312.5 312.5 312.5

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50 TPMPKRLXGKVAIVTGGARGIGEAIVRLFXKHGAXVVIADIDDAAGEALAXALGPX-VXF 108
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                65 IHCDVTNEDGVKNAVDNTVS-TYGKLDIMFSNAGI---SDPNRPRIIDNEKADFERVLSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 TAFARRIEGKVALITGGASGIGETTAKLFSQHGAKVALADVQDELGHSVVEAIGTSNSTY
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                                                                                                                                   219 AGNLKGPKFNVEDVANAALYLASDEAKYVSGHNLFIDGGFSVCNSVI 265
                                                                        285 LATIKGATURPRDIAEAALFLASDDSRYISGHNLVVDGGVTTSRNLI 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 359;
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Best Local Similarity 38.9%; Score 500; DB 1; Length 355
Best Local Similarity 38.8%; Pred. No. 1.3e-45;
Matches 112; Conservative 40; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                COPERATING STSIEM: PC-DOS/MS-DOS
SOFTWARE: PECENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,856A
FILING DATE: 15-MAY-1995
CLASSIFTCATION: 800
ATTORNEY AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,27
REFERENCE/DOCKET NUMBER: 05463-20001.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1517
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                                                                                                                                                                                                                                                                                                                                  ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 706141
INFORMATION POR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 359 amino acids
 182 OFGIRVNCLSPFGLPTAL-
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D.C.
USA
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121 NVTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVEL 180
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                                                                                                                                                                      286 RGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLI 334
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                                                                                                                                                                                                                                           TELERAX: (202) 887-0763
TELEX: 706141
INPORMATION FOR SEQ.
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acid
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APPLICANT: Rouviere, Pierre E.
APPLICANT: Brostowicz, Patricia C.
TITLE OP INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES FILE REFERENCE: BC1001 US NA CURRENT APPLICATION NUMBER: US/09/504,358
CURRENT APPLICATION NUMBER: 60/120,702
EARLIER APPLICATION NUMBER: 60/120,702
EARLIER FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Microsoft Office 97
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                                                                                          122 VTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGG--SSHAYCGSKHAVLALTRNLAVE 179
                                                                                                                                                                                                                                        180 LGQFGIRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYL 239
                                                                 STYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVN 121
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35.7%; Pred. No. 1.2e-31;
ive 55; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                               240 ASDEAKYVSGHNLFIDGGFSV 260
                                                                                                                                                                                                                                                                                                                                                      241 ASDLSAYLTGVTLDVNGGMLI 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/09504358
Patent No. 6365376
GENERAL INFORMATION:
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; ORGANISM: Brevibacterium sp HCU
US-09-504-358-14
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240 SFITGAVLPVDGGYT 254
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Best Local Similarity 35.7%
Matches 91; Conservative
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US-09-954-314-14
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Sequence 5747, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                                                                                                                  APPLICATE: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR PLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 RTAFARRLEGKVALITGGAS--GIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVNCLSPFGLPTALGKK-FSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI--GTSNSTYI
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  288 RGLATLKGXTLRPRDIAEAXLFLASDXXRYISGHNLVVDGGVTTSRNLI 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 31.4%; Score 437; DB 4; Length 30 I Similarity 37.9%; Pred. No. 6.6e-39; 96; Conservative 52; Mismatches 97; Indels
                                                                            9-09-252-991A-24032
Sequence 24032, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : :| | :||
285 GFTTGIALPVDGG 297
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Best Local Similarity 36.04
Matches 94; Conservative
                                                                                                                                                  GENERAL INFORMATION:
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US-09-328-352-5742
                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 24032
LENGTH: 301
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Best Local S
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us-09-673-918a-2.rai

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APPLICANT: SUGITAMA, MASAKAZU
APPLICANT: SUGITAMA, MASAKAZU
APPLICANT: TONOUCHI, NAOTO
APPLICANT: TONOUCHI, NAOTO
APPLICANT: SUZUKI, SUNICHI
APPLICANT: YOKOZEKI, KENZO
TITLE OF INVENTION: XYLITOL BHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
FILE REFERENCE: 0010-1034-0
CURRENT APPLICATION NUMBER: US/09/363,189B
CURRENT FILING DATE: 1998-07-26
RICH APPLICATION NUMBER: UP10-216047
RICH APPLICATION NUMBER: UP10-216047
NUMBER: OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.0
LENGTH: 262
TYPE: PRT
                                                                                                                                                                                                                                                     Sequence 773.1 Application US/09328352

Sequence 773.2 Application US/09328352

Patent No. 656298

GENERAL INFORMATION:
TITLE OF INVENTION: BULGEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BULGEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BULGEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BULGEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NOS: 8252
                                                                 65 VYDEDAYKQAIELIQKTFGTVDILINNAGFQ--HVAPIEEFPIAVFQKLVQVMLTGAFIG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 CLSPFGLPTALGK-----KFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLAS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.3%; Score 352; DB 4; Length 261; Best Local Similarity 34.5%; Pred. No. 8.2e-30; Matches 89; Conservative 53; Mismatches 104; Indels 1
                                  189 CLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 6, Application US/09363189B; Patent No. 624222B; GENERAL INFORMATION:
                                                                                                                                                   231 ASQLSSYMTAQTLVVDGGLT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Acinetobacter baumannii
US-09-328-352-7731
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US-09-363-189B-6
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TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES FILE REFERENCE: EGIOGI US NA CURRENT APPLICATION NUMBER: US/09/954,314
CURRENT PILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: 60/120,702
PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49
SOCTHWARE: Microsoft Office 97
SEQ ID NO 14
LENGTH: 256
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US-09-198-452A-309
US-09-198-452A-309
US-09-198-452A-309
Sequence 309, Application US/09198452A
Federate No. 6559294
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prever TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
NUMBER OF SEQ ID NOS: 6849
LENGTH: 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNV---EDVANAALYLASDEA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                         10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI-GTSNS-TYIHCD
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                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                    Length 256;
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I Similarity 35.7%; Pred. No. 1.2e-31.
91; Conservative 55; Mismatches 101; Indels
                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Brevibacterium sp HCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-309
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US-09-954-314-14
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Best Local S:
Matches 87,
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Best Local S
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242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
                              Sequence 29, Application US/09468738A Patent No. 6312933
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                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                           US-09-468-738A-29
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                                                                                                                                                                               IRVNCLSP-------FGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKF-NVED 231
                                                                                                                                                                                                                                                                                                   180 IRVNAISÞGYMGPGFMWERQVELQAKVGSQYFSTDPKVVAQQMI---GSVPMRRYGDINE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 IHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTG 124
                                                                                                                                                                                                                      125 VFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFG 184
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                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDEL---GHSVVEAIGTSNSTY
                                                                                                                      APPLICANT: Wada, Masaru

TITLE OF INVENTION: Levodione reductase gene and use thereof
FILE REFERENCE: Levodione reductase
CURRENT APPLICATION NUMBER: US/09/773,748

CURRENT FILING DATE: 2001-01-31

PRIOR PILING DATE: 2000-02-01

NUMBER OF SEQ ID NOS: 2

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 267
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                                            25.1%; Score 349.5; DB 3; Length 3
31.2%; Pred. No. 1.5e-29;
ive 55; Mismatches 107; Indels
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1 Similarity 33.3%; Pred. No. 7.1e-29;
88; Conservative 48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                           232 VANAALYLASDEAKYVSGHNLFIDGG 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Corynebacterium aquaticum
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 1, Application US/09773748; Patent No. 6534297; GENERAL INFORMATION:
ORGANISM: Gluconobacter oxydans
                                                                         83; Conservative
                                                           Best Local Similarity
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Best Local Similarity
Matches 88; Conserv
    ; OKGANISM: GIL
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GENERAL INFUGRATION:

GENERAL INFUGRATION:

APPLICANT: Kimoto, No. 6312933ihiro

APPLICANT: Kimoto, No. 6312933ihiro

APPLICANT: Kimoto, Hiroaki

APPLICANT: Kimoto, Hiroaki

APPLICANT: Witsuhashi, Kazuya

TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING ALCOHOL USING SAI

TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAI

TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAI

TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAI

TITLE OF INVENTION: 1999-12-21

CURRENT FILING DATE: 1999-12-21

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-06-17

PRIOR FILING DATE: 1999-12-21

NUMBER: OF SEQ ID NOS: 29

SEQ ID NO 29

LENGTH: 261

LENGTH: 261
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APPLICANT: Kimoto, No. 6416986ihiro
APPLICANT: Kimoto, Hiroaki
APPLICANT: Wamamoto, Hiroaki
APPLICANT: Misuhashi, Kazuya
TITLE OF INVENTION: MOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING ALCOHOL USING SAI
TITLE OF INVENTION: ENCODING SAID ENZYME, AND METHOD FOR PRODUCING ALCOHOL USING SAI
TITLE OF INVENTION: ENZYME
FILE REPERENCE: 06501-05001
CURRENT APPLICATION WHBER: US/09/940,019
CURRENT APPLICATION NUMBER: 09/468,738
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 09/468,738
PRIOR APPLICATION NUMBER: JP 1998-361130
PRIOR APPLICATION NUMBER: US/09/96.361130
PRIOR FILING DATE: 1999-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GAFLGSREAIKYFVENDIKGNVINMSSVHEVIPWPLFVHYAASKGGIKLMTETLALEYAP 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 KGIRVNNIGPGAINTPINAEKFADPKOKADVESMIPM-GYIGEP----EEIAAVAAWLAS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 LKGKVVAITGAASGLGKAMAIRFGKEQAKVVINYYSNKQDPNEVKEEVIKAGG--EAVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LEGKVALITGGASGIGETTAKLFSQHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTYI
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SEQ ID NO 29
LENGTH: 261
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24.5%; Score 341.5; DB 4
Best Local Similarity 34.4%; Pred. No. 1.1e-28;
Matches 93; Conservative 50; Mismatches 98
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Sequence 5042, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/064,964
FRIOR FILING DATE: 1997-08-14
SEQ ID NOS: 5674

LENGTH: 267

LENGTH: 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 IHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGI--SDPNRPRIIDNEKADFERVLSVNV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 TGVFLCMKHAARVMIPA-RSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 FLSSDLASYIHGTTLYVDGG------MMNYP 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 YLASDEAKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
                                          242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
                                                                             234 KEASYVIGITLFADGGMT------QYP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: October 23, 2003, 12:52:01 Job time : 30 secs
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US-09-134-001C-5042
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APPLICANT: KIMOLO, NO. 6485948ihiro
APPLICANT: KIMOLO, NO. 6485948ihiro
APPLICANT: KIMOLO, NO. 6485948ihiro
APPLICANT: KIMOLO, NO. 6485048ihiro
APPLICANT: KIMOLOMICO, HILORKI
APPLICANT: MISHABARI, KAZAUMA
TITLE OF INVENTION: NOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING ALCOHOL USING SAI
TITLE OF INVENTION: ENZYME
FILE REPERENCE: 06501-05001
CURRENT APPLICATION NUMBER: 09/468,738
PRIOR APPLICATION NUMBER: 09/468,738
PRIOR APPLICATION NUMBER: 09/468,738
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
PRIOR PILING DATE: 1999-12-21
SEQ ID NOS: 29
LENGTH: 261
SEQ ID NOS: 29
LENGTH: 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 FGIRUNCLSPFGLPTAL-GKKFSGIKONEEFENVINFAGNLKGPKFNVEDVANAALYLAS 241
                                                                                                                                                                                                                                                                        GVFLCMKHAARVMIPAR-SGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQ 182
                                                                                                                                                                                                                                              66 HCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEK--ADFERVLSVNVT 123
                                                                                                                                                                                                                                                                                                                              124 GVFLCMKHAARVMIPAR-SGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQ 182
                                                                                                                                                                                           11 LEGKVALITGGASGIGETTAKLFSQHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTYI 65
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                                                                                                                         29; Gaps
                                                                               ch 24.5%; Score 341.5; DB 4; Length 261; l Similarity 34.4%; Pred. No. 1.1e-28; 93; Conservative 50; Mismatches 98; Indels 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/09940037A; Patent No. 6485948; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Bacillus subtilis
US-09-940-037A-29
    ; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-940-019-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-940-037A-29
                                                                                    Query Match
Best Local S
Matches 93
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Sequence:

Minimum DB Maximum DB

Database

Searched:

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STYIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: secoisolariciresinol dehydrogenase amino acid
OTHER INFORMATION: sequence from plasmid pAP1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lewis, No. US20020174452Alman
APPLICANT: Lewis, No. US20020174452Alman
APPLICANT: Lewis, No. US20020174452Alman
APPLICANT: ... Huang, Ning
TITLE OF INVENTION: Monocot Seeds with Increased Lignan
FILE REPERENCE: WSUR117983
CURRENT APPLICATION NUMBER: US/09/944,160
CURRENT APPLICATION NUMBER: US 60/230,632
PRIOR APPLICATION NUMBER: US 60/230,632
PRIOR APPLICATION NUMBER: US 60/230,632
PRIOR PILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FASESEQ for Windows Version 4.0
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Best Local Similarity 88.2%; Pred. No. 3.7e-115;
Matches 240; Conservative 14; Mismatches 18;
US-10-242-574-82
US-10-243-421-82
US-10-243-422-82
US-10-243-422-82
US-10-244-164-82
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US-10-245-104-82
US-10-245-104-82
US-10-238-183-82
US-10-238-183-82
US-10-238-183-82
US-10-245-771-82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
    US-09-944-160-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-944-160-24
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LENGTH: 276
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Sequence 11842, A
Sequence 11842, A
Sequence 14255, A
Sequence 14, Appl
Sequence 14, Appl
Sequence 6, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 82, Appli
                                                                                           October 23, 2003, 12:50:44; Search time 68 Seconds (without alignments) 672.305 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCCMB.pep:*
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              GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-342-224-8

US-10-1156-761-1135

US-10-156-761-11425

US-10-230-52-14

US-09-962-134-14

US-09-902-853-6

US-10-307-385-6

US-10-307-385-6

US-10-307-385-6

US-10-307-385-6

US-10-307-385-6

US-10-307-385-6

US-10-307-385-6

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US-10-327-48-1

US-10-327-48-1

US-10-327-48-1

US-10-242-074-82
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Maximum Match 100%
Listing first 45 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                           Sequence 8, Application US/1034224
| Publication No. US20030162294A1
| GENERAL INFORMATION |
| GENERAL INFORMATION |
| APPLICANT: Nathalie Verbruggen |
| TTUE OF INVENTION: Genes Involved in Tolerance to Environmental Stress |
| FILE REFERENCE: CNN-01210 |
| CURRENT APPLICATION NUMBER: US/10/342,224 |
| CURRENT PILING DATE: 2003-01-13 |
| PRIOR APPLICATION NUMBER: US/09/762,154 |
| PRIOR FILING DATE: 2003-02-02 |
| PRIOR FILING DATE: 1998-08-04 |
| NUMBER OF SEQ ID NOS: 123 |
| SEQ ID NO 8 |
| SEQ ID NO 8 |
| LENGTH: 272
                                                                                                 69 VTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 IKHAAKAMIKGGRGGSIICTSSSSGLMGGLGGHAYTLSKGGINGVVRTTECELGSHGIRV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 NCLSPFGLPT----ALGKKFSGIK-NEEFFENVINFAGN-LKGPKFNVEDVANAALYLA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 VIGVFLFMKHAARIMVPARSGCIISTASLSSTMGGGSSHAYCGSKHAVLGLTRNLAVELG 184
                                                                           182 QFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLAS 241
VTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 KRLFEKVAIITGGARGIGAATARLFTENGAYVIVADILIDNEGILVAESIG---GCYVHCD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68
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35.0%; Score 487.5; DB 12; Length
Best Local Similarity 44.2%; Pred. No. 1.6e-40;
Matches 118; Conservative 45; Mismatches 91; Indels
                                                                                                                                                                          245 DEAQYVSGQNLFIDGGFSVCNSAIKLFQYPDS 276
                                                                                                                                                    242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS 273
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; Parent No. US/005061569A1
; APPLICANT: Haselbeck, Robert
; APPLICANT: Oblsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Tawkick, John D.
; APPLICANT: Tawkick, John D.
; APPLICANT: Yamanoto, Robert T.
; APPLICANT: Yamanoto, Robert T.
; APPLICANT: Yamanoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-342-224-8
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RVNCLSPFGLPTALGKK-FSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLASDEA 244
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         INVENTION: Identification of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
11.0%; Score 432; DB 9;
Best Local Similarity 37.5%; Pred. No. 5.2e-35;
Matches 95; Conservative 52; Mismatches 98;
TITLE OF INVENTION: Identification of Essenti
TITLE OF INVENTION: Prokaryotes
FILE REFERNCE: ELITTA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-21
PRIOR PILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: 60/200,848
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-110-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-02-16
NUMBER: OF SEQ ID NOS: 14110
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APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIRBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: JAFARYOSHI
APPLICANT: JAFARYOSHI
APPLICANT: JAFARYOSHI
APPLICANT: MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
CURRENT FILLOG DATE: 249-262
CURRENT FILLOG DATE: 2002-05-29
PRIOR PELING DATE: 2001-05-30
PRIOR PELING DATE: 2001-05-30
PRIOR PELING DATE: 2001-05-30
PRIOR PELING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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Publication No. US20030119018A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 253
FYPE: PRT FT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11842
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US-10-156-761-11335
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US-09-954-314-14

US-09-954-314-14

Sequence 14, Application US/09954314

Sequence 14, Application US/09954314

Sequence 14, Application US/09954314

Setent No. USSO02012766641

APPLICANT: Rouviere, Pierre E.
APPLICANT: Brostcwicz, Patricia C.
TITLE OF INVENTION: GENERAL NA BAZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954,314

CURRENT APPLICATION NUMBER: 60/120,702

PRIOR FILING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49

SOFTWARE Microsoft Office 97

SEQ ID NO 14

LENGTH: 256
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                                                 68 DVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 CMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 NCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNV---EDVANAALYLASDEA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Brzoscowicz, Patricia C
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
TITLE OF INVENTION: UNTERMEDIATES
FILE REPERBYCE: BC-1001
CURRENT APPLICATION NUMBER: US/10/230,562
CURRENT APPLICATION NUMBER: US/10/230, 562
PRIOR PILING DATE: 1999-02-19
PRIOR FILING DATE: 1999-02-19
SOFTWARE: Microsoft Office 97
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.5%; Score 369; DB 10; Length 2 Best Local Similarity 35.7%; Pred. No. 1.1e-28; Matches 91; Conservative 55; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 14, Application US/10230562; Publication No. US20030113886A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Brevibacterium sp HCU
US-09-954-314-14
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                                                                                                                                          SCHNLFIDGGFS 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLCM 129
                                                                                                                                                                                                                                                                                                                                                                                                       130 KHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGOFGIRVNC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 LSPFGLPTALGKKFS---GIKNEEEFENVINFAGNL--KGPKFNVEDVANAALYLASDEA 244
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                                                                                                                                                                                                                         10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCDV 69
                                                                                                                                                                                                                                                     3 KLDGRVVLISGAARGGGEQEARLFVEEGAKVVVADVLDDQGEALAKEIG---ARYVHLDV 59
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                                                                                                                            27.4%; Score 382; DB 15; Length 2:
36.8%; Pred. No. 5.4e-30;
iive 46; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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larity 35.3%; Pred. No. 7.9e-30;
Conservative 48; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14255, Application US/10156761
FUDDICATION NO. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UUN
APPLICANT: HEBA, HARUO
APPLICANT: SHIRAWA, UUN
APPLICANT: SHIRAWA, HROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WSSHIRWI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, WSSHIRWI
ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 240-262
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 14255
LENGTH: 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 SYITGOPFVIDGGWLAGVSVI 258
                                          ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avermitilis
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Best Local Similarity
Matches 89; Conserv
                                                                                                                                                     Best Local Similarity
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SEQ ID NO 11335
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July 20-307-385-6

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July 20-307-385-6

July 20-307-385-7

July 20-307-308-7

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July 20-307-8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 IRVNCLSP-----FGLPTALGKKFSGIKNEBEFENVINFAGNLKGPKF-NVED 231
180 IRVNAISPGYMGPGFMWERQVELQAKVGSQYFSTDPKVVAQQMI---GSVPMRRYGDINE 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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; Sequence 1, Application US/09773748
; Publication No. US20020187537A1
; GENERAL INFORMATION:
; APPLICANT: Wada, Masaru
; TITLE OF INVENTION: Levodione reductase
; FILE REFRENCE: Levodione reductase
; CURRENT APPLICATION UNMBER: US/09/773,748
; CURRENT FILING DATE: 2001-01-31
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 267
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25.1%; Score 349.5; DB 15; Length:
Best Local Similarity 31.2%; Pred. No. 9.9e-27;
Matches 83; Conservative 55; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 VANAALYLASDEAKYVSGHNLFIDGG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 VANAALYLASDEAKYVSGHNLFIDGG 257
                                                                                  TYPE: PRT ORGANISM: Gluconobacter oxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-307-385-6
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| Sequence 6, Application US/09802853
| Patent No. US20010034049A1
| Sequence 6, Application US/09802853
| Patent No. US20010034049A1
| GENERAL INFORMATION:
| APPLICANT: SUGITYAM, MASKAZU
| APPLICANT: SUGITYAM, MASKAZU
| APPLICANT: SUGITYAM, WASKAZU
| APPLICANT: SUGITYAM, WASKAZU
| APPLICANT: YOKOZEKI, KENZO
| TITLE OF INVENTION: XYLITOL DEHYDROGENASE OF ACETIC ACID BACTERIA AND GENE THEREOF
| FILE REFERENCE: 010-1024-0
| CURRENT FILING DATE: 1909-07-12
| PRIOR APPLICATION NUMBER: US/363,189
| PRIOR APPLICATION NUMBER: UP/216047
| PRIOR FILING DATE: 1998-07-30
| WUMBER OF SEQ ID NOS: 16
| SOFTWARE: Patentin version 3.0
| LENGTH: 262
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                                                                                                                                                                                                                                                                                                                                                                                  IHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 VFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFG 184
                                                                                                                                                                                                                                                                                                                                                    68 DVINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 NCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNV---EDVANAALYLASDEA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
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                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                              10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN--STYIHC 67
                                                                                                                                                                                                                                                                                8 ARRLEGKVALITGGASGIGETTAKLFSOHGAKVAIADVQDEL---GHSVVEAIGTSNSTY
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25.1%; Score 349.5; DB 9; Length 262;
Best Local Similarity 31.2%; Pred. No. 9.9e-27;
Matches 83; Conservative 55; Mismatches 107; Indels 21.
                                                                                                                                         Length 256;
                                                                                                                                      26.5%; Score 369; DB 15; Length 2 35.7%; Pred. No. 1.1e-28; ive 55; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Gluconobacter oxydans
US-09-802-853-6
         ; LENGTH: 256
; TYPE: PRT
; ORGANISM: Brevibacterium sp HCU
05-10-230-562-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 KYVSGHNLFIDGGFS 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 SFITGAVLPVDGGYT 254
                                                                                                                                                                                             91; Conservative
                                                                                                                                            Query Match
Best Local Similarity
Matches 91; Conserv
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APPLICANT: Kimoto, No. US20020127679Alihiro
APPLICANT: Kimoto, No. US20020127679Alihiro
APPLICANT: Kimoto, Hiroaki
APPLICANT: Wamamoto, Hiroaki
APPLICANT: Misuhashi, Kazuya
TITLE OF INVENTION: MOVEL CARBONYL REDUCTASE, METHOD FOR PRODUCING SAID ENZYME, DNA
TITLE OF INVENTION: ENZYME
TITLE OF INVENTION: ENZYME
FILE REFERENCE: 05501-05001
CURRENT APPLICATION NUMBER: US/09/940,037A
FRIOR APPLICATION NUMBER: 09/468,738
FRIOR APPLICATION NUMBER: UP 1998-363130
FRIOR PILING DATE: 1999-12-21
RIOR APPLICATION NUMBER: UP 1998-13-21
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.0, reformatted using WordPerfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 HCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEK--ADFERVLSVNVT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GVFLCMKHAARVMIPAR-SGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQ 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LEGKVALITGGASGIGETTAKLFSQHGAKVAI---ADVQD--ELGHSVVEAIGTSNSTYI
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APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.5%; Score 341.5; DB 1
34.4%; Pred. No. 6.2e-26;
iive 50; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 DEAKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
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  241 VAFLLSDDASYVNATVVPIDGGQS 264
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Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
Wood, William
                                                                                                              ; Sequence 29, Application US/09940037A; Patent No. US20020127679A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 82, Application US/10237496
Publication No. US20030138896A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 34.48 Matches 93; Conservative
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APPLICANT: Eaton, Dan
APPLICANT: Filvaroff, Ellen
                                                                                          US-09-940-037A-29
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LENGTH: 261
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                               66 HCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEK---ADFERVLSVNV 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 FGIRVNCLSPFGLPTALGKKF-----SGIKNEEEFENVINFAGNLKGPKFNVEDVANA 235
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                                                                                                                                                                                                                    10 RFTDRVVLITGGGSGLGRATAVRLAAEGAKLSLVDVSSEGLEASKAAVLETAPDAEVLTT 69
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                                                                                                                                           Gaps
                                                                                                                                      Indels · 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/1032726
| Publication No. US20030138921A1
| GENERAL INPORMATION:
| APPLICANT: Wadd, Masaru
| TITLE OF INVENTION: Levodione reductase gene and use thereof
| FILE REFERENCE: Levodione reductase
| CURRENT FILING DATE: Loodione reductase
| CURRENT FILING DATE: 2002-12-23
| PRIOR APPLICATION NUMBER: US/10/327,726
| PRIOR PELING DATE: 2001-01-31
| PRIOR FILING DATE: 2001-01-31
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NOS: 2
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                                                                                             DB 10;
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                                                                                     Query Match 24.7%; Score 343.5; DB 10; Best Local Similarity 33.3%; Pred. No. 4.1e-26; Matches 88; Conservative 48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.7%; Score 343.5; DB 12;
larity 33.3%; Pred. No. 4.1e-26;
Conservative 48; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 ALYLASDEAKYVSGHNLFIDGGFS 259
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  ; TYPE: FRI
; ORGANISM: Corynebacterium aquaticum
US-09-773-748-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Corynebacterium aquaticum
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88; Conserv
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US-10-327-726-1
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Best Local S:
Matches 88,
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TYPE: PRT
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TITLE OF INVENTION: SECRETED AND TRANSMEWBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: 1963.081.019

CURRENT APPLICATION NUMBER: US/10/242,074

CURRENT FILING DATE: 2002-09-11

PRIOR FILING DATE: 1097-09-17

PRIOR PLICATION NUMBER: 60/059114

PRIOR PLING DATE: 1997-10-24.7

PRIOR APPLICATION NUMBER: 60/05027

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1997-11-10

PRIOR PLING DATE: 1998-03-27

PRIOR PLING DATE: 1998-03-27

PRIOR PLING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/086478

PRIOR PLING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/08667

PRIOR APPLICATION NUMBER: 60/08667

PRIOR PLING DATE: 1998-06-02

PRIOR PLING DATE: 1998-06-02
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Sequence 82, Application US/10242505
Publication No. US20030138898A1
GENERAL INFORMATION:
APPLICANT: Baten, Newin
APPLICANT: Flivancff, Ellen
APPLICANT: Gadard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Grimaldi, J. Smith, Smith, Victoria
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Flivaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephen, Jean-Phillippe
Watanbe, Colin
Wood, William
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232 VTGNPVIIDGGWSL 245
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CORGANISM: Homo Sapien
US-10-242-074-82
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Best Local Similarity
Matches 85; Conserv
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           CURRENT PELLING DATE: 2002-00-06
PRIOR APPLICATION NUMBER: US/10/237,496
PRIOR APPLICATION NUMBER: 10/197942
PRIOR PELLING DATE: 2002-00-18
PRIOR PELLING DATE: 2002-00-18
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-09-17
PRIOR PELLING DATE: 1997-10-24
PRIOR PELLING DATE: 1997-110-24
PRIOR PELLING DATE: 1998-03-27
PRIOR PELLING DATE: 1998-03-27
PRIOR PELLING DATE: 1998-03-27
PRIOR PELLING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: 60/08478
PRIOR PELLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08901
PRIOR APPLICATION NUMBER: 60/08901
PRIOR PELLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-18
PRIOR PELLING DATE: 1998-06-22
PRIOR PELLING DATE: 1998-06-28
PRIOR PELLING DATE: 1998-06-28
PRIOR PELLING DATE: 1998-06-25
PRIOR PELLING DATE: 1998-06-38
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23.8%; Score 332; DB 12; Length 245;
Best Local Similarity 33.5%; Pred. No. 5.1e-25;
Matches 85; Conservative 57; Mismatches 98; Indels 1
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Filvaroff, Ellen
Goddard, Audrey
Grimaldi, J. Christopher
Gurney, Austin
Smith, Victoria
Stephan, Jean-Phillippe
Watanbe, Colin
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232 VTGNPVIIDGGWSL 245
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APPLICANT: Baker Kevin
APPLICANT: Filvaroff.Bll
APPLICANT: Goddard, Audre
APPLICANT: Grimaldi,J. C
APPLICANT: Smith, Victori
APPLICANT: Smith, Victori
APPLICANT: Stephan, Jean-
APPLICANT: Watanbe, Colin
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Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
CORGANISM: Homo Sapien
US-10-237-496-82
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APPLICANT: Zhang, Zemin
APPLICANT: Fong, Sherman
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3630R.C25
CURRENT APPLICATION NUMBER: US/10/242,505
CURRENT PILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR PELIOR TOWNER: 60/063046
PRIOR FILING DATE: 1997-10-24
PRIOR FILING DATE: 1997-10-24
PRIOR PELIOR NUMBER: 60/063046
PRIOR PELIOR NUMBER: 60/06507
PRIOR PELIOR DATE: 1998-01-27
PRIOR PELIOR DATE: 1998-05-22
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
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232 VTGNPVIIDGGWSL 245
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Best Local Similarity
Matches 85; Conserva
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Search completed: October 23, 2003, 13:00:39 Job time : 69 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 23, 2003, 12:45:39; Search time 40 Seconds (without alignments) 656.351 Million cell updates/sec Run on:

Title: Perfect score:

US-09-673-918A-2 1393 1 MQLRTAFARRLEGKVALITG......IDGGFSVCNSVIKVFQYPDS 273 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		di			SUMMAKIES	
Result No.	Score	Query	Length	DB		Description
	734	52.7	267	. ~	/T11579	probable short cha
7	685	6	æ	7	T02257	
m	658.5	47.3	285	7	F96563	ical pr
4	625.5	44.9	0	7	T46064	short-chain alcoho
S.	597.5	42.9	æ	7	H85039	probable alcohol d
9	588.5	42.2	3	~	A47542	short-chain alcoho
7	575.5	41.3	9	7	T02174	probable alcohol d
80	567	40.7	S	7	T02175	
6	559	40.1	S	~	T06364	
10	549.5	σ	25	~	T02176	probable alcohol d
11	499.5	35.9	23	7	T03734	
12	490.5	ហ	27	~	T47354	alcohol dehydrogen
13	432	П	25	~	F83440	probable short-cha
14	402.5	28.9	S	N	C70885	probable dehydroge
15	398	ъ.	S	7	A10406	probable dehydroge
16	396	α	S	Н	839737	Н
17	386	27.7	S	7	G82644	2,5-dichloro-2,5-c
18	381.5	27.4	22	~	E72427	uctase
19	0	w	56	~	T36846	probable dehydroge
20	366	ø	9	~	H70758	probable fabG3 pro
21	363	26.1	4	~	H72219	3-oxoacyl-(acyl ca
22	363	26.1	S	0	AC1478	dehydrogenase/redu
23	363	ġ.	S	~	AI1117	dehydrogenase/redu
24	361.5	ø	σ	7	E87260	hypothetical prote
25	S	'n	4	7	H86527	oxoacyl (carrier p
56	S	25.6	4	7	D72096	3-oxoacyl-(acyl-ca
27	356.5	S	4	~	F83838	oxidoreductase (sh
28	S	വ	246	N	H84136	3-oxoacyl-(acyl-ca
53	353.5	25.4	α	N	F91082	probable oxidoredu

probable short chain alcohol dehydrogenase - common tobacco C;Species: Nicotiana tabacum (common tobacco) C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000 C;Accession: T02257 R;Herbers, K.; Moenke, G; Badur, R.; Sonnewald, U. Plant Mol. Biol. 29, 1027-1038, 1995 A;Title: A simplified procedure for the subtractive cDNA cloning of photoassimilate-respond A;Reference number: S62698; MUID:96145513; PMID:8555446

RESULT 2

probable oxidoredu	oxidoreductase, sh	dehydrogenase homo	dehydrogenase homo	oxidoreductase, sh	probable dehydroge	probable [imported	hypothetical prote	glucose 1-dehydrog	oxidoreductase, sh	glucose 1-dehydrog	hypothetical prote	hypothetical prote	hypothetical prote	probable 3-ketoacy	2-deoxy-D-gluconat
G85927	B82181	AB1717	AG1346	G72389	B65059	F95284	E87279	F69868	A72395	D69629	C87474	D90481	D70635	B97223	F69400
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N	~	~	N	(A		• •	C4	N	7	~	~	7	7	(1)	7
286 2	252 2	253 2	253 2	251 2	286 1	257	261 2	248 2	257 2	261 2	521 2	299 2	255 2	248 2	281 2
25.4 286 2	25.0 252 2	24.9 253 2		24.8 251 2										24.0 248 2	
25.4	348.5 25.0 252 2	24.9	24.9	24.8	24.8		24.7	24.6	24.5		24.5	24.3	24.1	24.0	

ALIGNMENTS

RESULT 111579 Probab- C, Space C, Date C, Acce R, Titll A, Refe A, Refe A, Refe A, Refe A, Statt A, Rele A, Crosi C, Supe	RESULT 1 T11579 Probable short chain alcohol dehydrogenase CPRD12, drought-inducible - cowpea C.Species: Vigna unguiculata (cowpea) C.Species: Vigna unguiculata (cowpea) C.Species: Os-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 20-Jun-2000 C.Accession: T11579 C.Accession: T11579 A.Fitle: Characterization of two cDNAs for novel drought-inducible genes in the highly do A.Fitle: Characterization of two cDNAs for novel drought-inducible genes in the highly do A.Fatus: preliminary; translated from GB/EMBL/DDBJ A.Accession: T11579 A.Accession: T11579 A.Accession: 1-267 < 1UC.> A.Residues: 1-267 < 1UC.> A.Cross -references: EMBL:D88121 C.Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
Quer	Query Match 52.7%; Score 734; DB 2; Length 267;
Best	Best Local Similarity 56.3%; Pred. No. 0.1e-51;
Matcl	Matches 147; Conservative 41; Mismatches 67; Indels 6; Gaps 2;
çy	9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD 68
G	
çy	69 VTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
Qa	: ::
Oy	129 MKHAARVMIBARSGNIISTASLSSTWGGSSHAYCGSKHAVLALTRNLAVELGGFGIRVN 188
Op	
Qy Dp	189 CLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKYVS 248
oy	249 GHNLFIDGGFSVCNSVIKVFQ 269
op	

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probable alcohol dehydrogenase [imported] - Arabidopsis thaliana probable alcohol dehydrogenase [imported] - Arabidopsis thaliana (mouse-ear cress) (5.8pecies: Arabidopsis thaliana (mouse-ear cress) (5.8pecies: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001 (5.8 Arabidopsis not that the sequence are also in the succession in the European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999 (Arabidopsis of chromosome 4 of the plant Arabidopsis thaliana. Argeference number: A85001; MUID:20083488; PMID:10617198 (Arabidopsis thaliana. Arsteus: preliminary Arbidocule type: DNA Ar
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NyAlcernate names: protein Tablidopsis thaliana
NyAlcernate names: protein Tablidopsis thaliana (mouse-ear crees)
CyBecies: Arabidopsis thaliana (mouse-ear crees)
CyBecies: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000
CyBeciession: T46064
RyDelseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, K.; Nubmitted to the Protein Sequence Database, December 1999
A;Recession: T46064
A;Recession: T46064
A;Recession: T46064
A;Residues: 1-303 AbEL
A;Residues: 1-303 AbEL
A;Residues: 1-303 AbEL
A;Residues: 1-303 CABEL
A;Residues: 1-303 CABEL
A;Residues: 1-303 CABEL
A;Residues: 1-303 CABEL
A;Cooserimental source: cultivar Columbia; BAC clone T18N14
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A,Introns: 31/2
A,Note: TIBN14.60
C,Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ---YIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGI--SDPNRPRIIDNEKADFERVL 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 TLYPKRLEGKVAIITGGAHGIGKATVMLFARHGATVVIADVDNVAGSSLAKSLSSHKTSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 EDVANAALYLASDEAKYVSGHNLFIDGGFSVCNSVI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 NDIAEAALYLASDESKYVNGHNLVVDGGVTTARNCV 301
                                                                                                                                                                                                                                                                                                   237 LYLASDEAKYVSGHNLFIDGGFSVCNSVIKVFQ 269
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Pyg6501

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Pyg
A;Accession: T02257
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-284 <HER>
A;Croser references: BMBL:AJ223177; NID:g2739278; PIDN:CAA11153.1; PID:g2739279
A;Experimental source: cultivar SNN; tissue-type leaf
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGIRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLASD 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 YIHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVT 123
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47.3%; Score 658.5; DB 2; Length 285;
Best Local Similarity 50.9%; Pred No. 8.6e-45;
Matches 139; Conservative 43; Mismatches 78; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                     Query Match

49.2%; Score 685; DB 2; Length 284;
Best Local Similarity 53.8%; Pred. No. 6.8e-47;
Matches 140; Conservative 37; Mismatches 83; Indels
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A;Gene: F14M4.3; At2g47140
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Matches 120; Conserv
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A; Introns: 163/2
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C;Species: Zea mays (maize)
C;Date: 03-may-1994 #sequence_revision 03-May-1994 #text_change 31-Mar-2000
C;Accession: A47542
R;DeLong, A.; Calderon-Urrea, A.; Dellaporta, S.L.
Call 74, 75-768, 1993
A;Title: Sex determination gene tasselseed2 of maize encodes a short-chain alcohol dehyd A;Reference number: A47542; MUID:93364991; PMID:8358795
A;Accession: A47542
A;Accession: A47542
A;Accession: A47542
A;Accession: A47542
A;Accession: A47542
A;Cossion: A47542
A
                                                                   A,Gene: AT4g03140
A,Map position: 4
C,Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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GB:NC_001268; NID:g7270184; PIDN:CAB77799.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHCDVINEDGVKNAVDNIVSTY-GKLDIMFSNAGI---SDPNRPRIIDNEKADFERVLSV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                   68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                  DB 2; Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 336;
                                                                                                                                                                                                                                                                                                                              86; Indels
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                                                                                                                                                                                                                                         Query Match 42.9%; Score 597.5; DB 2 Best Local Similarity 47.0%; Pred. No. 5.8e-40; Matches 126; Conservative 45; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKYVSGHNLFIDGGFSVCNSVIKVFQYP 271
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Best Local Similarity 42.2
Matches 122; Conservative
A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
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A Experimental Source: cultivar Columbia
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I
M.; Kao, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Accession: E84911
A;Accession: E84911
A;Amolecule type: DNA
                                                                                                                                                                                                                                                                                 M.; Ron
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                             NyAlternate names: hypothetical protein F14M4.3
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001
C;Accession: T02174; E84911
R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, Psubmitted to the EMBL Data Library, September 1998
A;Bescription: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
A;Reference number: 214609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-264 <STO>
A;Cross-references: GB:AE002093; NID:g3522952; PIDN:AAC34234.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable alcohol dehydrogenase At2g47130 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F14M4.4 (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Nam-1999 #text_change 16-Feb-2001 (Spacession: T02175; D84911 (Spacession: T02175) (Spacession: T021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVNCLSPFGLPTALGKKFSGIKNEEE-FENVINFAGNLKGPKFNVEDVANAALYLASDEA
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    Arabidopsis thaliana

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A;Scatus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 < ROU>
A;Residues: 1-264 < ROU>
A;Residues: EMBL:AC004411; NID:g3522932; PID:g3522952
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46.9%; Pred. No. 3e-38;
iive 49; Mismatches 82;
probable alcohol dehydrogenase [imported]
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probable alcohol dehydrogenase At2g47120 [imported] - Arabidopsis thaliana
NyAlernate names: hypothetical protein F14M4.5
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.
C;Accession: T02176
A;Ball Data Library, September 1998
A;Beernde number: Z1409
A;Reference number: Z1409
A;Reference number: Z1409
A;Reatus: translated from GB/EMBL/DDBJ
A;Reatus: translated from GB/EMBL/DDBJ
A;Reatus: translated from GB/EMBL/DDBJ
A;Reatus: creferences: EMBL:AC004411; NID:g3522932; PID:g3522936
A;Reatus: LySs -ROD,
A;Reatus: LySs -ROD,
A;Reatus: LySs -ROD,
A;Reatus: LySs -ROD,
A;Reatus: C; Rod, B; Rod,
A;Reatus: C; Rod,
A; Rod, C; Rod,
A; Rod,

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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 TNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLCM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KHAARVMI-PARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN 188
                                                                                                                                                                                                                                                                                                                       132 AARVMIPAR-SGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVNCL 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCDV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <STO-
A;Cross-references: GB:AE002093; NID:g3522936; PIDN:AAC34218.1; GSPDB:GN00139
C;Genetics:
          72 EDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLCMKH
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Best Local Similarity 44.5%; Pred. No. 3.3e-36;
Matches 113; Conservative 53; Mismatches 79; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 NLAVDGGLS---SILKL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 NLFIDGGFSVCNSVIKV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: At2g47120; F14M4.5
A,Map position: 2
A,Introns: 5/2
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A;Status: translated from GB/EMBL/DDBJ
A;Mclecule type: DNA
A;Mclecule type: DNA
A;Residues: 1257 <ROU4
A;Cxos-references: EMBL:AC004411; NID:g3522932; PID:g3522935
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 76-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reterence number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84911
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <STO
A;Cross-references: GB:AE002093; NID:g3522935; PIDN:AAC34217.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g47130; F14M4.4
A;Map postition: 2
A;Introns: 5/2
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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ToGASTA
C'SPECIES: Lycopersicon esculentum (tomato)
C'Species: Lycopersicon esculentum (tomato)
C'SACCESSION: TOGASTA
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TATLE: Gibberellins regulate the abundance of RNAS with sequence similarity to protein
A)ATLLE: Gibberellins regulate the abundance of RNAS with sequence similarity to protein
A)ACCESTA
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A)STATUS: DAGASTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKHAARVMI-PARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 NCLSPFGLPTALGKKFSGIKNEEEFENVINFA---GNLKGPKFNVEDVANAALYLASDEA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 TNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRP-RIIDNEKADFERVLSVNVTGVFLC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 EGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCDVTN 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.7%; Score 567; DB 2; Length 257;
Best Local Similarity 45.4%; Pred. No. 1.3e-37;
Matches 118; Conservative 49; Mismatches 81; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 40.1%; Score 559; DB 2; Length 251; al Similarity 47.5%; Pred. No. 5.6e-37; 122; Conservative 46; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 KYVSGHNLFIDGGFSVCNSV 264
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A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
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A;Cross-references: GB:AE004592; GB:AE004091; NID:g9947609; PIDN:AAG05038.1; GSPDB:GN001
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: PA1649
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83440
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, ..., Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                        VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                                                                                                                                                                                            MKHAARVMIP-ARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
                                                                                                                                                                                                                                                                                                                RVNCLSPFGLPTALGKK-FSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEA 244
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                                     RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
                                                                                                                                                                                                                                                                                                                                                                                                  NCLSPFGLPT----ALGKKFSGIK-NEEEFENVINFAGN-LKGPKFNVEDVANAALYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 ARRIEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI--GTSNSTYI
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probable dehydrogenase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
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31.0%; Score 432; DB 2;
Best Local Similarity 37.5%; Pred. No. 6.7e-27;
Matches 95; Conservative 52; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 SQESSGFITGHNLVVDGGYTSATSTMR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 SDEAK-YVSGHNLFIDGGFSVCNSVIK 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: F83440
A;Status: preliminary
A;Molecule type: DNA
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alcohol dehydrogenase (ATA1) - Arabidopsis thaliana
alcohol dehydrogenase (ATA1) - Arabidopsis thaliana
N;Alternate names: protein F18P9,120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C;Accession: T47354
R;Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.;
Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                        Short chain alcohol dehydrogenase homolog - common tobacco
NyAlternate names: TFHP-1 protein
Cispecieses: Nicototiana tabacum (common tobacco)
Cispecieses: Nicototiana tabacco, Nicotot
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A;Note: F18P9.120
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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GVAPYAVATPMTSHDEVTG----KQLEDYFDAKGILKGMVLKASHVAQVALFLASDDSAY 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGVFLCMKHAARVMIPARSG-NIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.9%; Score 499.5; DB 2; Length 2 Best Local Similarity 47.5%; Pred. No. 2.7e-32; Matches 112; Conservative 33; Mismatches 82; Indels
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A;Experimental source: cultivar Columbia; BAC clone F18P9
                                                        247 VSGHNLFIDGGFSV 260
                                                                                           A; Reference number: Z24458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Accession: T47354
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-272 < NYA>
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183
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M.J.; Br. K.; Lim,

125

61

185

(strain PAC

240

65 IHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGIS--DPNRPRIIDNEKA---DFERVLS 119 VNVTGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVE 179

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180 LGOFGIRVNCLSPFGLPTALGKK-FSGIKNEEEFENVINFAGNLKGP--KFNV-EDVANA 235
                                                                                                                                                                                                                                                                          180 WGPLDIQVNAISPTVVITALGQKAWSGQLAEDM------KLKIFPARRFAYPAEVAAC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                        completed: October 23, 2003, 12:51:25
ne : 42 secs
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A10406
probable dehydrogenase YPO3351 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Accession: A10406
R;Parkhill, J.; Wren, B. W.; Thomson, N. R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
Geno-Tarraga, A.M.; Cillingworth, T.; Cronin, A.; Sevens, K.; Whitehead, S.; Barrell,
Nature 413, S23-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Recession: A10406
A;Status: preliminary
A;Molecule type: DMA
A;Residues: 1-256 <kUR>
A;Cross-references: GB:ALS90842; PIDN:CAC92581.1; PID:g15981278; GSPDB:GN00175
C;Gentics:
A;Gente: YPO3351
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C; Accession: C70885
R; Colloss, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M., Ragers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J. B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A; Feference number: A70500; MUD1: 98295897; PMD1: 9634230
A; Reference number: A70500; MUD1: 98295897; PMD1: 9634230
A; Reference number: DA
A; Recession: C70885
A; Status: prellminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DA
A; Residues: 1-258 «COLD.
A; Richors references: CB: AL008883; GB: AL123456; NID: 93261490; PIDN: CAA15519.1; PID: 9261280
                                                                                                                                                                                                                                                                                                                                                                                                                          A;Geme: Rv2857c
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;11-188/Domain: short-chain alcohol dehydrogenase homology <5ADH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMKHAARVMIPARSGNIISTASLSSTMGGGSSH-AYCGSKHAVLALTRNLAVELGOFGIR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNCLSPFGLPTALGKKFSGIKNEEFFENVINF-AGNLKGPKFNVEDVANAALYLASDEAK 245
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Best Local Similarity 37.4%; Pred. No. 3.4e-24;
Matches 99; Conservative 51; Mismatches 87; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 28.9%; Score 402.5; DB 2; Length 258; Best Local Similarity 35.8%; Pred. No. 1.5e-24; Matches 91; Conservative 49; Mismatches 105; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 FITASTFLVDGGIS 251
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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- protein search, using sw model OM protein October 23, 2003, 12:38:34; Search time 23 Seconds (without alignments) 558.187 Million cell updates/sec Run on:

US-09-673-918A-2

1393 1 MQLRTAFARRLEGKVALITG......IDGGFSVCNSVIKVFQYPDS 273 score: Perfect sc Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 seqs, 47026705 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB 8 Maximum DB 8

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SwissProt_41:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	381.5	7	25	Н	Y019 THEMA		ga
ល	376	7	25	Н	LINX PSEPA		าลธ
φ	366	9	56	٦	YK02 MYCTU		əri
7	363	9	24	٦	FABG THEMA		ä
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6	346	4	25	7	Y325_THEMA	-	'a
10	345.5	4	56	ч	YGCW_ECOLI		ıia
11	343.5	24.7	56	7	LVR LEIAQ		e e
12	341.5	24.5	56	٦	DHG_BACSU		ສຸດ
13	334	24.0	25	Н	Y4MP RHISN		8
14	332.5	23.9	24	-	FABG CHLMU		E
15	332	23.8	263	Н	UCPA_SALTY	P37441 salmonella	la
16	329.5	23.7	27	7	LIMC RHOER		Sno
17	328.5		IJ	Н	DHSO_RHOSH		er
18	326.5		4	Н	FABG_CHLTR	chlamyc	a د
19	320.5		4	Н	FABG_VIBCH	vibrio	chol
50	320.5		9	Н	YXBG_BACSU	P46331 bacillus	Bu
21	m		2	Н	2BHD STREX		/ce
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23	315.5	22.6	9	Н		_	me
24	m		~	Н		flavoba	cter
25	314.5		9	-	DHG1_BACME	P39482 bacillus	шe
56	m		4	н	FABG_RICPR	P50941 rickettsia	i,a
27	310		9	Н	UCPA_ECO57		nia
28	m		ø	Н	UCPA_ECOLI	_	nia
29	o	•	9	Н	DHGA_BACME	bacillu	me
30	8		4		FABG SALTY	085141 salmonell	la
31	8		9	7		P39483 bacillus	me
32	m	22.1	9	Н		9071 bacillu	ns
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P39484 bacillus me P39485 bacillus me	P51831 bacillus su Q51576 pseudomonas	P25529 escherichia P42317 bacillus su	Q00791 emericella P07914 eubacterium	P07999 bacillus me P73574 synechocyst	P19337 eubacterium P50199 gluconobact
DHG3_BACME DHG4_BACME	FABG_BACSU YV06_PSEAE	HDHA_ECOLI	STCU_EMENI BA71_EUBSP	DHGB_BACME FAG1_SYNY3	BA72_EUBSP GNO_GLUOX
	н н				
261 261	246 255	255	264	262	249
22.0	21.9	21.8	21.6	21.2	21.2
306.5	305.5	303 302	301	296	295
34 35	36 37	38 38	4 4 0 1	4 4 2 8	4 4 5

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47 TPMPKRLDGKVAIVTGGARGIGEAIVRLFAKHGARVVIADIDDAAGEALASALGPQVS-F 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 TAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVALADVQDELGHSVVEAIGTSNSTY 64
                                                                                                                                                                                                                                                                                                                                                                                                   cent 4::>,-res(1935).
-i-FUNCTION: REQUIRED FOR STAGE-SPECIFIC FLORAL ORGAN ABORTION.
-i- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                              STRAIN=Cv. W22;
WEDLINE=23464991; PubMed=8358795;
Delong A., Calderon-Urrea A., Dellaporta S.L.;
Mesx determination gene TASSELSEED2 of maize encodes a short-chain alcohol dehydrogenase required for stage-specific floral organ
                                                                                                                                                 Zea mays (Maize).
Skaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42.2%; Score 588.5; DB 1; Length 336;
42.2%; Pred. No. 1.5e-39;
tive 50; Mismatches 88; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MaizeDB; 56963; ...
Interpro; IPR002199; ADH short.
Pfam; PR01016; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
Oxidoreductase; Developmental protein.
NP BIND 83 NAD OR NADP (BY SIMILARITY).
ACT_SITE 207 207 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4E273D6152B0BB99 CRC64;
                                                     01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
Sex determination protein tasselseed 2.
                     336 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L20621; AAC37345.1; -. PIR; A47542; A47542.
HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 42.2%
Matches 122; Conservative
                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                          abortion.";
Cell 74:757-768(1993)
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                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SDR) family.
                                                                                                                                                                                                                        NCBI_TaxID=4577;
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                   TS2 MAIZE P50160;
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SEQUENCE
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TS2 MAIZE
ID TS2 M
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NEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLCMK 130
                                              131 HAARVMIP-ARSGNIISTASLSSTWGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVNC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                             180
                                                                                                                                                                                       225
       IHCDVTNEDGVKNAVDNTVSTY-GKLDIMFSNAGI----SDPNRPRIIDNEKADFERVLSV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=UT25;
MDDLNE=9422977; PubMed=7515041;
MSGRA T. Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2,5-dichloro-2,5-cyclohaxadiene-1,4-diol
dehydrogenase gene involved in the degradation of gamma-
hexachlorocyclohaxane in Pseudomonas paucimobilis.";
J. Bacteriol, 176:317-3125 (1994).
I. PUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL.
(2,5-DDCL) INTO 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL.
(3,5-DDCL) INTO 2,5-DICHLORO-3,5-DCHO).
I. PATHWAY: Gamma-hexachlorocyclohexane degradation; third step.
(SDR) family.
                                           LSGKTIIVTGGGSGIGRATVELLVASGANVPVADINDEAGEAVVATSG-GKAAYFRCDIA
                                                                                                                                                                                                                                                           -----LGKKFSGIKNEEEFENVI
                                                                                                                                                                 NVTGVFL CMKHAARVMI PARSGNI I STASLSSTMGGGSSHAY CGSKHAVLALTRNLAVEL
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29.1%; Score 406; DB 1; Length 250;
Best Local Similarity 37.9%; Pred. No. 3.2e-25;
Matches 96; Conservative 42; Mismatches 103; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
1-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria, Proteobacteria, Alphaproteobacteria, Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
NCBI_TaxID=13689;
                                                                                                                                                                                                                                                                                                                                                                                                                     286 RGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLI 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D14595; BAAA...
HSSP; P19992; JHDC.

(InterPror, IPRO02108; ADH_short.)

R PRINTS; PRO0106; SDRFAMILY.

R PRINTS; PS00060; SDRFAMILY.

R PROSITE; PS000601; ADH_SHORT; 1.

R Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.

9 34 NAD.

14 SA SIMILARITY.

15 A SIMILARITY.

16 T-14 NW; FFCICAEB47DF789D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  217 NFAGNLKGPKFNVEDVANAALYLASDEAKYVSGHNLFIDGGFSVCNSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 AA.
                                                                                                                                                                                                                                                           181 GOFGIRVNCLSPFGLPTA------
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Kunet F., Ogdaawara N. Moscar I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Barriss R., Boursier L., Brans A., Braun M., Brignells C.C., Bron S.,
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Rochis S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
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Britz C., Fujita M., Fujita Y., Fuma S., Galizil A., Galleron N.,
A dimeppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A dimeppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A dimeppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
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A doris B., Karamata D., Kashara Y., Klaerr-Blanchard M., Klein C.,
A doris B., Koetter P., Koningstein G., Manol C., Medigue C.,
A kuita K., Lapidus A., Liu H., Masuda S., Manol C., Medigue C.,
A kuita K., Lapidus A., Liu H., Masuda S., Manol C., Medigue C.,
A hee S.M., Levine A., Liu H., Masuda S., Manol C., Medigue C.,
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A preseen E., Pully C., Rocha E., Rapoport G., Rey M., Sadaie Y.,
A resecon E., Scanlan E., Schleich S., Schroeter R., Scoffons F.,
Sator T., Scanlan E., Schleich S., Schroeter R., Scoffons F.,
Schiguchi J., Sekowska A., Serror P., Shin B.S.,
Sekiguchi J., Sekowska A., Serror P., Shin B.S.,
A rewell M., Taaconl E., Takagi T., Takahashi H., Takemaru K.,
A Takeuchi M., Tamakeshi A., Tanaka T., Terpstra P., Toganori A.,
A Takeuchi M., Tamakeshi A., Serror P., Shin B.S.,
A viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
A Takeuchi M., Tamaka H.F., Zumstein E., Yoshikawa H., Danchin A.,
A voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H.F., Zumstein E., Weitzen E., Wedler E., We
LSPFGLPTALGKKFSGIKNE---EFFENVINFAGNLKGPKFNVEDVANAALYLASDEAKY 246
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NCBL_TaxID=1423;
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01-FEB-1995 (Rel. 31, Last sequence update)
02-FEB-2003 (Rel. 41, Last annotation update)
Hypothetical oxidoreductase ywfD (EC 1.-.-)
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                                                                                                                                                                                                                                                                                                                                                                                                   247 VSGHNLFIDGGFS 259
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DY PEBBO
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DT 28-FEBD
DE YWFD 01
CS Bacter
OC NCBIT
RA BACIDIN
RA GLISSE
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RA RADOPO
RT "BACIDIN
RA MEDLIN
RA MIDSE
RA GUISSE
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 NEDGVKNAVDNTVSTYGKLDIMFSNAGIS--DPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||| :|| || || || || || SKHALKHMLAAGKGNIINTCSVGGLVAWPDIPAYNASKGGVLQLTKSMAVDYAKHQIRVN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLSPFGLPTALGKKFSGIKNEEEFENV-----INFAGNLKGPKFNVEDVANAALYLASD 242
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subtilis.";
Nature 390:249-256(1997).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
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STRAIN=MSB8 / DSM 3109;
MEDLINE=96125254; PubMed=8550425;
Kletzin A., Adams M.;
"Molecular and phylogenetic characterization of pyruvate and 2-
ketoisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus
and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
J. Bacteriol. 178:248-257(1996).
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBI_TaxID=2336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.4%; Score 396; DB 1; Length 25 36.6%; Pred. No. 2e-24; ive 48; Mismatches 99; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE, PS00061; ADH SHORT; 1.

Hypothetical protein; Oxidoreductase; Complete proteome.

NP BIND 11 33 NAD OR NADP (BY SIMILARITY)

ACT_SITE 154 154 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20AA2259BFB88C9B CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-CTT-2010 (Rel. 40, Least annotation update)
Putative oxidoreductase TM0019 (EC 1.-.-.)
                                                                                                                                                                                                                                                                                                          EMBL, 299123; CAB15799.1; -. P.R., S39737, S39737, S39737, S39737, S39737, S39737, S39737, S39737, S401629; JAEL. SUBTILIST, BGGG, BGGG, SAM, SHORT, PRANTS; PRO0106; adh SHORT; PRINTS; PRO00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 LSSYMTGSAITADGGYT 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255 AA; 27324 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94; Conservative
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                                                                                       Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS--NSTYIHCD
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01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase (EC 1.1.-.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; NADP; Complete proteome.
NADP (BY SIMILARITY).
BY SIMILARITY.
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28078 MW; D68160B1D7980C6B CRC64;
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SEQUENCE FROM N.A.
STRAIN=MSB8 / DSM 3109;
MEDLINE=99287316; PubMed=10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
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153
136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; E72427; E72427.
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TIGR; TM0019; -.
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                                                                                                                                                                                                                                                                                                                                                                                                           (SDR) family.
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MEDIATE=922977; PubMed=7515041;
MEDIATE=9252977; PubMed=7515041;
Magata Y., Ohtomo R., Miyauchi K., Fukuda M., Yano K., Takagi M.;
"Cloning and sequencing of a 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase gene involved in the degradation of gamma-hexachlorocyclohexane in Pseudomonas paucimobilis.";
J. Bacteriol. 176:3117-3125(1994)
-!-PUNCTION: DEGRADATION OF 2,5-DICHLORO-2,5-CYCLOHEXADIENE-1,4-DIOL (2,5-DDOL) INTO 2,5-LICHLOROHYDROQUINONE (2,5-DCHQ). LINX IS NOT ESSENTIAL TO GAMMA-HCH DEGRADATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTS--NSTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Degradation of gamma-hexachlorocyclohexane.
SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                              Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
Sphingomonadaceae; Sphingomonas.
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HSSP; P1992; 1HDC.
INCEPERO; IPROC1298; ADH_short.

R FEam; PP00106; adh short; 1.

R PRINTS; PR00080; SDRFAMILY.

R PRINTS; PR00080; ADH_SHORT; 1.

R PR00080; ADH_SHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.0%; Score 376; DB 1; Length 250;
.larity 36.2%; Pred. No. 7.6e-23;
Conservative 49; Mismatches 90; Indels 3
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TO VROS MYCTU

TO Q10855,

DT 01-0CT-1996 (Rel. 34, Created)

T 15-VUL-1999 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annocation update)

DE Putative oxidoreductase Rv2002 (EC 1....).
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Les 96; Conserv
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SDR) family.
                                                                                                                                   NCBI_TaxID=13689;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 KHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVNC 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterston J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Rolonay J.F., Nalson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 RLEGKVALITGGASGIGETTAKLFSQHGAKVALADVQDELGHSVVEAIGTSNSTYIHCDV
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S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
                                                                                                                                                      MEDLINE=98295997; PubMed=9634230;
MEDLINE=98295997; PubMed=9634230;
MEDLINE=98295997; PubMed=9634230;
Gordon S. V., Broan R., Parkhill J., Garnier T., Churcher C., Harris I Gordon S. V., Eiglmeier K., Gas S., Barry C. E. III, Tekaia F., Badcock K., Basham D., Erown D., Chillingworth T., Connor R., Badcock K., Devlin K., Peltwell T., Gentles S., Hamilin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Sulston J.E., Taylor K., Skelton S., Squares S., Squares R., Sulston J. E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 274025; CAA96814.1; -.
EMBL; AE007057; AAK46335.1; -.
EMBL; AE007057; AAK46335.1; -.
EMBL; ANOTS8; H70758;
EDB; INFR; 04-MAR-03.
FIGR; MT2058; -.
TUBCTULISE; RV2002; -.
TUBCTULISE; RV2002; -.
FEM; PF00106; adh_short.
Ffam; PF00106; adh_short.
FRAM; PF00106; ABHSHORT; 1.
FROSTE; PS00061; ADH SHORT; 1.
Hypothetical protein; Oxidoreductase; NAD; Complete proteome;
                    Mycobacterium tuberculosis.
garceria, Actinobacteria, Actinobacteridae, Actinomycetales;
Corynebacterineae, Mycobacteriaceae, Mycobacterium.
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Local Similarity 34.7%; Pred. No. Se-22;
Les 91; Conservative 42; Mismatches 87; Indels
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0935A14ED36220B7 CRC64;
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OR RV2002 OR MT2058 OR MTCY39.16C
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153 153 BY
174 174 S
260 AA; 27030 MW;
                                                                                                                     SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=1773;
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RAVVKPMKEAGRGSIINISSIEGLAGTVACHGYTATKFAVRGLTKSTALELGPSGIRVNS 180
                                                LSPFGL-----PTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANA 235
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                                                                                                                                                                                                                                              Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey B.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Bisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
PATHWAY: Fatty acid biosynthesis pathway. First reduction step. SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                        Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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BY SIMILARITY.
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                                                                                                                                                                                                                      246 AA
                                                                             IHP-GLVKTPMTDWVPEDIFQTALGRAAEPV-
                                                                                                           236 ALYLASDEAKYVSGHNLFIDGG 257
                                                                                                                                       216 VVYLASDESSYSTGAEFVVDGG 237
                                                                                                                                                                                                                      PRT;
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
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FABG OR TM1724
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                                                                                                                                                                                                                                                                                                      SUTTOMINE STATEMENT STATEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 VNAVAPGFIETPMTEKLPEKARETALSRIP--LGRFGKP----BEVAQVILFLASDESSY 232
67 CDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVF 126
                                                                                                                                                                                                                              LCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIR 186
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (BC 1.1.1.100) (3-ketoacyl-acyl-carrier-protein reductase)
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                                                                        UNCLSPFGLPTALGKKFSGIKNEEFFENVINFACNLKGPKFNVEDVANAALYLASDEAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314 (2000).
-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-oxoacyl-[acyl-carrier protein] + -!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ą.
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MEDLINE=99206606; PubMed=10192388;
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                                                                                                                                                                                                                                                                                                                                                                                                            129 MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN 188
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STRAINEMES J DSW 3109;
MEDLINE=9287316; PubMed=10360571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Hafck D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Pleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999)
-!-SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                                                              123 CSSVIRHMIKARSGSIINVASIVAKIGSAGQTNYAAAKAGIIAFTKSLAKEVAARNIRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLAPGFI------ETDMTSVLN--DNLKAEWLKSIPLGRAGTPEDVARVALFL
                                                                                                                                                                                                                                                                                               11 LEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI-GTSNS-TYIHCD
                                                                                                                                                                                                                                                                                                               CLSPFGLPTALGKKFSG1KNEEEFENVINFAGNLK------GPKFNVEDVANAALYL
                                                                                                       TIGK; COMBA; ADH Short.

Pfam; PF00106; adh Short; 1.

PRINTS; PR00106; DRFAMILY.

PROSITE; PR000061; ADH SHORT; 1.

PROSITE; PR000061; ADH SHORT; 1.

NP BIND 12 36 NADP; Complete proteome.

ACT SITE 156 156 BY SIMILARITY).
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                    ch 25.6%; Score 357; DB 1; .iength 248; I Similarity 33.5%; Pred. No. 2.4e-21; 87; Conservative 53; Mismatches 92; Indels ;
                                                                                                                                                                                                            01A2A758B701577E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Hypothetical oxidoreductase TM0325 (EC 1.-..).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AA
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                                                                                                                                                                                                            248 AA; 26504 MW;
EMBL; AE001614; AAD18445.1; --
BMBL; AE002207; ARE38299.1; --
BMBL; AP002346; BAA98506.1; --
PIR; H86527; H86527; H86527;
HSSP; P19992; 1HDC.
PHCI. ZDPAGE; Q928P2; --
IIGR; CP0462; --
IIGR; CP0462; --
IIGR; CP0462; --
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NCBI TaxID=2336;
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Best Local S
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 AKD--AEQIVKKTVETFGRLDILVNNAGIVPYG--NIEETSEEDFDKTMAVNVKGPFLLS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190 LSPFGLPTALG--KKFSGIKNEEEFENVINFAGNLK--GPKFNVEDVANAALYLASDEAK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 TNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLCM 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 KHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVNC
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BIDLINE-27149980; PubMed-9205837;
Yamamnco Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoco Y., Aiba H., Baba T., Hayashi K., Miki T., Mitsuhashi N.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
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SEQUENCE FROM N.A.
STAALN*LAZ / MGJES5;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rlay M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tocherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 24.8%; Score 346; DB 1; Length 251; Local Similarity 36.9%; Pred. No. 1.8e-20; Loservative 45; Mismatches 100; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                         EMBL, AE001714; AAD35412.1; -.
PIR, G72389; G72389; G72389; T228; TMS2P; P50162; LAE1.
TIGR; TW0022; PF0002198; ADH_short.
InterPro; IPR002198; ADH_short.
PFIMI, PF000060; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
PROSITE; PS00061; ADH_SHORT; 1.
ACT_SITE 152 152 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61C736A0F13564A5 CRC64;
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01-NOV-1997 (RR1 35, Created)
101-NOV-1997 (RR1 35, Last sequence update)
16-OCT-2001 (Rel. 35, Last annotation update)
Hypothetical oxidoreductase ygcW (EC 1.-.-)
YGCW OR B2774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 YVSGHNLFIDGG 257
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236 FMTGSIINIDGG 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  251 AA;
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AC P7663
DT 01-NOV
DT 01-NOV
DT 16-OCT
DN YGCW C
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OC BECKET
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ACT_SITE
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                  11 LEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHS--VVEAIGTSNSTYIHCD 68
                                                                                                                                                                                                                                                                                                                                                                                                                               the Escherichia coli
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia col-KL2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                 HSSP1, LEGGRE, BG13130; yggw.
RECOGENE; EG13130; yggw.
RILEEPEO; IPR002198; ADH_short.
R Pfam; PF00106; adh short; 1.
R PRINTS; PR00080; SDRPAMILY.
RROSITE; PS00080; ADH SHORT; 1.
RROSITE; PS000061; ADH SHORT; 1.
RWOSITE; PS000061; ADH SHORT; 1.
RWD OR NADP (BY SIMILARITY).
166 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                     24.8%; Score 345.5; DB 1; Length 261; 32.3%; Pred. No. 2.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leifsonia aquatica (Corynebacterium aquaticum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Levodione reductase (BC 1.1.1.-) ((6R)-2,2,6-trimethyl-1,4-
cyclohexanedione reductase).
                                                                                                                                                                                                                                                                                                                                                                                            58; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Micrococcineae, Microbacteriaceae, Leifsonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 AA
                                                                                                                                                                                                       EMBL; U29579; AAA69285.1; ALT_INIT.
EMBL; AE000361; AAC75816.1; ALT_INIT.
EMBL; D90893; BAA16569.1; ALT_IÑIT.
HSSP; P25529; 1AHH.
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247 VNGHLLVVDGGYLV 260
                                                                                                                                                                                                                                                                                                                                                                                Similarity 32.3
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                           (SDR) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 VADVSDEAQVEAYVTATTERFGRIDGFFNNAGIEGKQNP----TESFTAAEFDKVVSINL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGVFLCMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGO 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (actinol).
CATALYTIC ACTIVITY: (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone
                        Yoshisumi A., Wada M., Takagi H., Shimizu S., Nakamori S., "Cloning, sequence analysis, and expression in Escherichia coli of the gene encoding monovalent cation-activated levodione reductase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22638325; PubMed=12621044; Sogabe S., Yoshizumi A., Fukami T.A., Shiratori Y., Shimizu S., Sogabe S., Yoshizumi A., Fukami T.A., Shiratori Y., Shimizu S., Takagi H., Nakamori S., Wada M., The crystal structure and stereospecificity of levodione reductase from Corynebacterium aquaticum M-13."; J. Biol. Chem. 278:19387-19395(2003).
-: FUNCTION: Catalyzes the regio. and stereoselective reversible NAD-dependent reduction of (6R)-2,2,6-trimethyl-1,4-cyclohexanedione (1evodione) to (4R,6R)-4-hydroxy-2,2,6-trimethylcyclohexanone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           + NAD(+) = (6R)-2,2,6-trimethyl-1,4-cyclohexanedione + NADH.
-!-RNZYME REGULATION: Strongly activated by monovalent cations, such as K(+), Na(+), and NH4(+).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wada M., Yoshizumi A., Nakamori S., Shimizu S.;
"Purification and Characterization of monovalent cation-activated
levodione reductase from Corynebacterium aquaticum M-13.";
Appl. Environ. Microbiol. 65:4399-4403(1999)
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E->A,D,N,Q: 26-fold increase in Km
much lower enantiomeric excess of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 343.5; DB 1; Length 267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD (BY SIMILARITY).
BY SIMILARITY.
Role in the determination of
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                                                                                                                               Čorynebacteríum aquaticum M-13.";
Biosci. Biotechnol. Biochem. 65:830-836(2001)
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                                                                                                                                                                                                                                          PARTIAL SEQUENCE, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                          STRAIN=M-13;
MEDLINE=99437825; PubMed=10508066;
MEDLINE=21281640; PubMed=11388460;
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HSSP; P19992; 1HDC.
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165
103
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nes 88; Conserv
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RAGIORNE FROW N.A.

RAGE STRAIN=168;

RADINES 98044033; PubMed=9384377;

RADINES PROBLE C.V., Brans A., Braun M., Brignell S.C., Brons S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Radiolo S.K., Codani J.J., Comnerton I.F., Cummings N.J., Daniel R.A., Chois S.K., Codani J.J., Publer B. C., Ebrlich S.D., Emmerson P.T., RADINGS P. C., Pruita M., Fulita Y., Puble S. M., Colaines D.J., Gaffeau A., Golightly B.J., Garlaci D., Carter N., Golightly B.J., Garlaci D., Carter D., Coffeau A., Golightly B.J., Graddi G., Guiseppi G., Rashara Y., Rollaga K., Hancot A., Golightly B.J., Harwood C.R., Henaut A., A doise D., Kashara Y., Koningstein G., Krogh S., Kumano M., Jones L., A doise M., Lading A., Lading A., Lader D., Lazarevic V., Lading A., Lading A., Lading S., Mauel C., Medigue C., Robaysshi Y., Kochteelle D., Rasuber J., Ladber G., Radina N., Mallado R.P., Diradinois S., Lauber J., Lazarevic V., Radio S., Radio B., Radio B., Persecan E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Reger M., Ravolta C., Rocha B., Roch B., Rose M., Sacro S.J., Serror P., Shin B.S., Soldo B., Tokato J., Jakenchi M., Tamakoshi A., Taramata T., Takahashi H., Takamashi H., 
                                                                     183 FGIRVNCLSPFGLPTALGKKF-----SGIKNEEEFENVINFAGNLKGPKFNVEDVANA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97124189; PubMed=8969502; Yamano K., Kurita K., Tumano K., Kurita E., Kurita R., Manano M., Kurita R., G., Kumano M., Kurita R., G., Kumano M., Kurita R., G., Kumano M., Kurita R., Getermination of the sequence of a 146 kb segment and identification of 113 genes. ", G. 113 genes.", Microbiology 142:3047-3056 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Madblinse-Bef168021, PubMed=3082854;
Lampel K.A., Uratani B., Chaudhry G.R., Ramaley R.F., Rudikoff S.,
"Characterization of the developmentally regulated Bacillus subtilis
glucose dehydrogenase gene.";
Jucose dehydrogenase gene.";
G. Bacteriol. 166:238-43(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                       P12310; P94430;
01-OCT-1989 (Rel. 12, Created)
30-MX7-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucose 1-dehydrogenase (EC 1.1.1.47).
                                                                                                                                                 236 ALYLASDEAKYVSGHNLFIDGGFS 259
                                                                                                                                                                                                             241 VAFLLSDDASYVNATVVPIDGGQS 264
                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GVFLCMKHAARVMIPAR-SGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQ 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 LKGKVVAITGAASGLGKAMAIRFGKEQAKVVINYYSNKQDPNEVKEEVIKAGG--EAVVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
  lactone + NAD(P)H.
-!- SUBUNIT: Homotetramer.
-!- INDUCTION: IT INDUCTION: TIS INDUCED AT STAGE III OF THE SPORULATION.
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Putative short-chain type dehydrogenase/reductase Y4MP (EC 1.-.-.).
CATALYTIC ACTIVITY: Beta-D-glucose + NAD(P)(+) = D-glucono-1,5-
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                                                                                                                                                                                                                                                                                                                                                                                      Plasmid sym pNGR234a.
gacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 KEASYVTGITLFADGGMT-----QYP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 24.5%; Score 341.5; Local Similarity 34.4%; Pred. No. 4.4e es 93; Conservative 50; Mismatches
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SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
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                                                                                                                                                                                                                                                                                                                        EMBL; M12276; AAA22463.1; -.
EMBL; D50453; BAA09024.1; -.
EMBL; Z99106; CAB12201.1; -.
PIK; D69629; D69629.
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UCPA_SALTY
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SEQUENCE
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Matches
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         177 FGPDSIRVNCVTPGLIQTDITGDKLSAEMRADIVKGIPLSRLGDAR-----DVANIYL 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLCMKHAARVMIPAR----SGNIISTASLSSTMGGG--SSHAYCGSKHAVLALTRNLAVE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 L----NLSQVFIPNMRQNGGGSIACMSSVSAQRGGGIFGGPHYSAAKAGVLGLAKAMARE 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 LGQFGIRVNCLSPFGLPTAL-GKKFSGIKNEEFFENV-INFAGNLKGPKFNVEDVANAAL 237
                                                                                                                                                                                                                                                                                                                                                                          LEGKVALITGGAS --GIGETTAKLFSQHGAKVAIADVQ-DELGHSVVEAIGTSNSTYI-- 65
                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase).
FABG OR TCOSO8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=MoPn / Nigg;
MEDLINE=20150525; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W.,
Eisen J., Praser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                           HCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGV
                                                                                                                                                                                                                                                                                                                                                   26; Gaps
              Perret X.;
"Molecular basis of symbiosis between Rhizobium and legumes.";
Mature 387:394-401(1997).
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
(SDR) FAMILY: HIGH, TO BACTERIAL FABG.
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                         24.0%; Score 334; DB 1; Length 253; 34.2%; Pred. No. 1.7e-19; ive 55; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                 92; Indels
                                                                                                                                                                                                                                                                        NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                B8208A0B0F5F542F CRC64;
                                                                                                                                                                                                                     PERMYS; PRO0106; adh short; 1.
PRINTS; PRO0080; SDRPAMILY.
PROSTIE; PS00061; ADH SHORT; 1.
PROSTIE; PS00061; ADH SHORT; 1.
NPOETHELICAL protein; Oxidoreductase; Plasmid.
NP_BIND 10 35 NAD OR NADP (BY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 YLASDEAKYVSGHNLFIDGGFSV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLASDLSAYVTGAVIDVNGGMLI 252
                                                                                                                                                                                                           InterPro; IPR002198; ADH short.
                                                                                                                                                                                   EMBL; AE000085; AAB91779.1; -.
                                                                                                                                                                                                                                                                                                  25994 MW;
                                                                                                                                                                                                                                                                                                                                  l Similarity 34.2
90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                     159 1
253 AA;
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SEQUENCE
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Best Local
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: | | | :: ||: ||: || |: : |: : || ||: ||: ||: ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : : ||: : : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : : ||: : : ||: : : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||: : ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVINEDGVKNAVDNTVSTYGKLDIMFSNAGIS-DPNRPRIIDNEKADFERVLSVNVTGVF 126
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                                                           pneumoniae AR39.";
Nuclaic Acids Res. 28:1397-1406(2000).
Nuclaic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-!- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
-!- SATHWAY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
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Enterobacteriaceae, Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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sequences of Chlamydia trachomatis MoPn and Chlamydia
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SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Oxidoreductase ucph (EC 1....).
UCPA OR STY245 OR STY2682 OR T0413.
Salmonella typhimurium, and
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PEam; PF00106; Adh short; 1.
PRINTS; PR00009; SDRRAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE002319; AAF39350.1; -.
PIR; E81695; E81695.
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TIGR; TC0508; -.
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nes 85; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
SPECIES=S. LYPhi; STRAIN=CT18;
SPECIES=S. LYPhi; STRAIN=CT18;
Barkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Whitehead S., Barrell B.G.,
Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.Lyphi, STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18."
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.; Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                               of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 185:2330-2337(2003).
-!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases (SDR) family.
                                                                                                                                                                                                        SPECIES=S.typhimurium;
MEDINE=91358382; PubMed=1909324;
MEDINE=91358382; PubMed=1909324;
MEDINE=91358382; PubMed=1909324;
MITALIES OF M.M., Kredich N.M.;
"The cysp promoter of Salmonella typhimurium: characterization of binding sites for CysB protein, studies of in vivo transcription initiation, and demonstration of the anti-inducer effects of thiosulfatee.";
J. Bacteriol. 173:5876-5886(1991).
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33.1%; Pred. No. 2.5e-19;
iive 49; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BY SIMILARITY).
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258 S -> T (IN REF. 2).
27870 MM, 81826CAD984D534E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, AECO8810, AALZ1339 11; --
EMBL, AECO8110, AALZ1339 11; --
EMBL, AECO16835, AACO8131.1; --
FIR, A38121, A38121, A38121, A38121, A38121, EVGene, SGI0424; ucpA.
InterPro, IPR002198; AbH short.
Fram, PF00106; adh short.
FROSITE; PS00061; ADH_SHORT; FALSE_NGG.
OXIGORGACEGUESE, COMPLETE PS00061; ADH_SHORT; AND OR NADP CR.
AND OXIGORGACEGUESE.
                                                                                                                                                                                            SEQUENCE OF 204-263 FROM N.A.
                                                                                                                                                  Nature 413:852-856(2001)
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218
258
258
263 AA;
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Best Local S
Matches 87
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CONFLICT
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Gaps

14;

Length 263;

Similarity 33.1 87; Conservative

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| : |: || : ||: ||: :|||: ...|| | CNDFASVQAAVARAKETEGRIDILVNNAGVCRLGNFLDMSEEDRDFH--IDINIKGVWNV 120
                                                                                                                                                                                              121 TKAVLPEMIKRKDGRIVMMSSVTGDWVADPGETAYALSKAAIVGLTKSLAVEYAQSGIRV 180
                                                                                                                                                                                                                                                         188 NCLSPFGLPTALGKKFSGIKNEEEFENVINFAG-----NLKGPKFNVEDVANAALYLAS 241
                                                                                                                                                                                                                                                                                    3 KLTGKTALITGASQGIGEGIARVFARHGANLILLDISDEIEKLADELGGRGHRCTAVKAD 62
RLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSN-STYIHCD
                                                                                 VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC
                                                                                                                                                                       129 MKHAARVMIPARSGNIISTASLSSTM-GGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV
                                                                                                                                                                                                                                                                                                                                                                      237 DESSYLTGTQNVIDGGSTLPESV 259
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completed: October 23, 2003, 12:48:56 ne : 26 secs Search co Job time

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October 23, 2003, 12:45:14 ; Search time 97 Seconds (without alignments) 726.272 Million cell updates/sec
                                                                                                                                                                                                      US-09-673-918A-2
1393
1 MQLRTAFARRLEGKVALITG......IDGGFSVCNSVIKVFQYPDS 273
                                                                                                                                                                                                                                                                                                                                                                                                      830525
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                       830525 seqs, 258052604 residues
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Maximum Match 100%
Listing first 45 summaries
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2: sp_arches:*
3: sp_bacteria:*
4: sp_human:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
9: sp_phage:*
10: sp_plane:*
11: sp_vordent:*
12: sp_virus:*
13: sp_vortebrate:*
14: sp_unclassified:*
15: sp_rus:*
16: sp_bacteriap:*
17: sp_archeap:*
18: sp_archeap:*
19: sp_archeap:*
11: sp_archeap:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

					SUMMARIES	
Result		Ouerv				
No.	Score	Match	Match Length DB	DB	ID	Description
	1364	97.9	277	នុ	Q94KL7	094kl7 forsythia i
7	734	52.7	267	10	P93697	P93697 vigna ungui
m	700.5	50.3	271	10	Q94G09	Q94g09 cucumis sat
4	695	49.9	274	10	600н80	Oshods phaseclus l
ß	693.5	49.8	271	10	Q94G10	094q10 cucumis sat
ė	685	49.2	284	10	050038	050038 nicotiana t
7	677	48.6	284	10	082465	082465 ipomoea tri
ω	673	48.3	277	10	Q9SBD8	09sbd8 ipomoea tri
6	670	48.1	284	10	Q9SBD6	
10	668	48.0	277	10	Q9SBD7	09sbd7 ipomoea tri
11	665.5	47.8	273	10	Q9SBM0	_
12	658.5	47.3	285	10	Q9C826	Q9c826 arabidopsis
13	652.5	46.8	278	10	Q94KL8	Q94kl8 podophyllum
14	625.5	44.9	303	10	OSSCIO OSSCIO	
15	597.5	42.9	283	10	Q9ZR17	Q9zr17 arabidopsis
16	593.5	42.6	259	10	Q93Y47	

		oryza s	oryza sa	oryza			Q91s70 arabidopsis		Q94k41 arabidopsis	080713 arabidopsis	arabid	O	Ф	-	Q8lid5 oryza sativ	Q8lid6 oryza sativ	arabidops	pisum sat	pisum sat	Q8lic5 oryza sativ	zea	Q94fd0 zea mays su	Q93vx4 zea mays su	9 zea	zea	zea	ED.	zea
91.МЗ	P93795	QBLIC3	Q8LIC2	Q8LIB8	QBLIC4	Q9LEG3	Q9LS70	Q8LIB9	Q94K41	080713	Q9LW34	QBLIC1	Q941E4	Q40133	Q8LID5	08LID6	080714	Q9SQF9	095013	QBLICS	Q94FC9	Q94FD0	Q93VX4	Q93W09	Q93VX5	Q93W75	Q93W76	Q94FC7
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17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

PRELIMINARY; PRT; 277 AA. 2001 (TrEMBLrel. 19, Created) 2003 (TrEMBLrel. 19, Last sequence update) 101 intermedial (Border forsythia) 102 intermedial (Border forsythia) 103 (TrEMBLrel. 20, Last sequence (Fragment). 103 (TrEMBLrel. 20, Last sedicotyledons; core eudicots; 104 (Vidiolpantae; Streptophyta; Embryophyta; Tracheophyta; 105 lamids; Lamiales; Oleaceae; Forsythia. 105 lamids; Lamiales; Oleaceae; Forsythia. 108 (Annial Sapiest H.C., Davin L.B., Lewis N.G.; 109 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. ImPLICATIONS FOR HUMAN HEALTH PROTECTION."; 101 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. ImPLICATIONS FOR HUMAN HEALTH PROTECTION."; 101 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. ImPLICATIONS FOR HUMAN HEALTH PROTECTION."; 101 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. ImPLICATIONS FOR HUMAN HEALTH PROTECTION."; 101 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. ImPLICATIONS FOR HUMAN HEALTH PROTECTION."; 100 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. 101 lariciresinol Dehydrogenase Purification, Cloning, and Expression. 102 lariciresinol Dehydrogenase Purification, Cloning, and anal Expression. 103 lariciresinol Dehydrogenase Purification, Constraints 103 lariciresinol Dehydrogenase Purification, Constraints 103 lariciresinol Dehydrogenase Purification, Constraints 104 lariciresinol Dehydrogenase Purification, Constraints 105 lariciresinol Dehydrogenase Purification, Constraints 107 lariciresinol Dehydrogenase Purification, Constraints 108 lariciresinol Dehydrogenase Purification, Constraints 109 lariciresinol Dehydrogenase Purification,	RESULT 1 D 094KL7 AC 01-DEC- DT 01-DEC- CC BETTICLINE RA XIS Z.C. RT SECULINE RA XIS Z.C. RT SECULINE RA XIS Z.C. CC -!- SIN CC -!-
	94KL7; 94KL7; 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 1-DEC-20 10 TOE-2 1-DECEDENCE 1-DECEDENC

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Q94G09
AC Q94G09;
DT Q1-DEC-DT O1-DEC-DT O1-DE
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        121
                                 STYIHCDVINEDGVKNAVDNIVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVFSVN 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKYVS 248
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                                                                                                        VTGVFLCMKHAARVMI PARSGNI I STASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p93697;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
CPRD12 procedin.
CPRD12 procedin.
Bukaryota, Viriaiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
NCbl_TaxID=3917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Iuchi S., Yamaguchi-Shinozaki K., Urao T., Shinozaki K.;

"Characterization of two cDNAs for novel drought-inducible genes in the highly drought-tolerant cowpea.";

J. Plant Res. 109:415-424(1996).

-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 267;
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EMBL; D88121; BAA1341.1; -.

INTERFY: D89292; LHDC.

INTERFY: PRO0106; adh short.

PRON176; pro0060; adh short; 1.

PROSTITE; PS00601; ADH_SHORT; 1.

SEQUENCE 267 AA; 28484 MW; 8C4A48A2E9F41B64 CRC64;
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                                                                                                                                                                                                                                                                                                                                      DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS 277
                                                                                                                                                                                                                                                                                                    DEAKYVSGHNLFIDGGFSVCNSVIKVFQYPDS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 AA.
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Best Local Similarity 56.33
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 NSTYIHCDVINEDGVKNAVDNIVSTYGKLDIMFSNAGI--SDPNRPRIIDNEKADFERVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 ELGQFGIRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLK-GPKFNVEDVANAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MOLRTAFARRIEGKVALITGGASGIGETTAKLFSOHGAKVAIADVODELGHSVVEAIGTS
                                                                                                                                                   Cucumis sativus (Cucumber).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Cucurbitales; Cucurbitaceae; Cucumis.
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Sun J.-Q., Li Q.-Z., Li X.-G.;
Sun J.-Q., Li Q.-Z., Li X.-G.;
Sun J.-Q., Li Q.-Z., Li X.-G.;
Gene cloning and expression of CSG in cucumber.";
Submitted (JUL-2000) to the EMBL/GenBank/DBBJ databases.
-1. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
EMBL. AF286651; AAK83036.1; -.
INTERPO: IPRO02198; ADH short.
PERM: PRO0106; adh short; 1.
PRINTS: PRO0060; SDRRAMIT; 1.
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Horiuchi J., Arimura G., Ozawa R., Muroi A., Takabayashi J.,
Nishioka T.;
"Phaseolus lunatus.";
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 50.3%; Score 700.5; DB 10; Length Best Local Similarity 33.7%; Pred: No. 376-45; Indels Matches 146; Conservative 44; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase.
SEQUENCE 271 AA; 28997 MW; 7CD6ED7F52AD6224 CRC64;
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Last sequence update)
Last annotation update)
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                                                                  Last sequence update)
Last annotation update)
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271 AA
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Q8H0D9 (2003) (TrEMBLrel. 23, C1
01-MAR-2003 (TrEMBLrel. 23, Li
01-MAR-2003 (TrEMBLrel. 23, Li
Alcohol dehydroge. 23, Li
                                           01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                          Sex determination protein.
CSG.
  PRELIMINARY;
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66 IFVHCNVAVESDVQNVVDATIAKFGKLDIMFSNAGIGGKSISSILDVDYDIIKTVFDVNI 125
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  179 ELGQFGIRVNCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLK-GPKFNVEDVANAAL 237
                                    182 DLGRYGIRVNCVSPNVVPTEMGRKLFKVKDGGEFP---SFYWSLKNGDILREEDVGEAVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leaf;
MEDLINE=9614513; PubMed=855446;
MEDLINE=9614513; PubMed=855446;
"A simplified procedure for the subtractive cDNA cloning of photoassimilate-responding genes: isolation of cDNAs encoding a new class of pathogenesis-related proteins.";
Plant Mol. Biol. 29:1027-10138(1995).
-i - SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                 Nicotiana tabacum (Common tobacco)
Skaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.2%; Score 685; DB 10;
53.8%; Pred. No. 5.9e-44;
ive 37; Mismatches 83;
                                                                                                                   239 YLGSDESKCVSGLNLIVDGGFTVVNOALCSFR 270
                                                                                           238 YLASDEAKYVSGHNLFIDGGFSVCNSVIKVFQ 269
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                                                                                                                                                                                                                                                                                                                                                       Short chain alcohol dehydrogenase. SCANT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DSKYVSGMNLVIDGGFSTTN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SDR) FAMILY.

EMBL, AJ223178; CAA11154.1; -.

EMBL, AJ223177; CAA11153.1; -.

HSSP, P19992; 1HDC.

InterPro; IPR002198; ADH short.

Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 EAKYVSGHNLFIDGGFSVCN 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH SHORT; 1.
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Best Local Similarity 53.8*
Matches 140; Conservative
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moenke G.;
Submitted (DEC-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase
                                                                                                                                                                                                                                                                                                       01-JUN-1998
                                                                                                                                                                                                                                                                                                                        01-JUN-1998
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVNVTGVFLCMKHAARVMIPARSCNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
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                                                                                                                                                                                                                                                     IHCDVTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTG
                                                                                                                                                                                                                                                                               5 TAFARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTY
                                                                                                                                                                                    VFLCMKHAARVMI PARSGNI I STASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGOFG
                                                                                                                                                                                                                                                                                                                                                                                                                                         IRVNCLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLASDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cucumis sativus (Cucumber).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.

NCBI_TaxID=3659;
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Sun J.-Q., Li Q.-Z., Li X.-G., Zhang X.-S.;

"Gene cloning and expression of CTA in cucumber.";

"Submitted (JUL.-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.8%; Score 693.5; DB 10; Length 271; 53.3%; Pred. No. 1.3e-44;
                                                                   Length 274;
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75; Indels
EMBL; AB086039; BAC53872.1; -.
SEQUENCE 274 AA; 28862 MW; DEC858BDB324877F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AA; 28931 MW; 8C5C5603CCCB49B4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                            69;
                                                                   10;
                                                                49.9%; Score 695; DB 10;
54.8%; Pred. No. 9.9e-45;
ive 42; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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EMBL; AF266650; AAK83035.1; -.

InterPro; IPR002198; ADH short.

Pfam; PF0106; adh short; 1.

PRINTS; PR00080; SDRPAMILY.

PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 NYVSGHSLLLDGGYTITNA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KYVSGHNLFIDGGFSVCNS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 19, C
(TrEMBLrel. 19, I
(TrEMBLrel. 23, I
                                                                                      Best Local Similarity 54.8
Matches 142; Conservative
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Matches 145, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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01-DEC-2001 (
01-MAR-2003 (
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                                                              Query Match
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094G10
1D 094G1
DT 01-DB
DT 01-DB
DT 01-DB
DT 01-DB
DT 01-M
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DT 01-M
DD 01-DB
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DD 01-DB
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DD 01-DB
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 DVRIESDVQNAVDTTVSRYGKLDIMFSNAGVAGSRDTSILEASPENINLVFETNVFGAFF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CMKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRV 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKYV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KOWYSMA Y., KAdota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T., Kowysma Y., Kadota N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T., Kowysma Y., Norioka S., Sassa H., Kassa S., Sassa S., Norioka S., Sassa S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ipomoea trifida.
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
Asteridae, lamiida; Solanales; Convolvulaceae; Ipomoea.
VCBI_TaxID=35884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Convolvulaceae; Ipomoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ttch 48.6%; Score 677; DB 10; Length 284; al Similarity 51.9%; Pred. No. 2.4e-43; 135; Conservative 41; Mismatches 84; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 AA; 29823 MW; 4C04A88B178C0633 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9SBD8;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Short-chain alcohol dehydrogenase.
                                                                                                                                                                                                        (TrEMBLrel. 08, Created)
(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                            Short-chain alcohol dehydrogenase.
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                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=35884;
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01-MAR-2003
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Best Local S
Matches 135
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132 AKHAARVMIPARKGSVIFSASAASEVFGITSDTYTASKCAVVGLCKSLCVEMGKYGIKAN 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
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Kowyama Y. Kadora N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T., Kondo K., Norioka S.; Settler Statement Stateme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVALADVQDELGHSVVEAIGTSNSTYIHCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eŭkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Asteridae, lamids, Solanales, Convolvulaceae, Ipomoea. NCBI_TaxID=35884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
48.3%; Score 673; DB 10; Length 2'
Best Local Similarity 51.7%; Pred. No. 4.6e-43;
Matches 134; Conservative 42; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 AA; 29312 MW; 7A75BEF12A73D9AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Short-chain alcohol dehydrogenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 GHNLFIDGGFSVCNSVIKV 267
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69 VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 AKHAARVMIPEKNGCILFTSSATTNIAGLSSHPYAASKCAVLGLVRNLAAELGQHGIRVN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRIESDVQNAVDTTVSRYGKLDIMFSNAGVAGSRDTSILEASPENINLVFETNVFGAFFC
                                                                                                              CLSPFGLPTALGKKFSGIKN----EEFFENVINFAGNLKGPKFNVEDVANAALYLASDEAK
12 KRLEGKVAIITGAANGIGATTARLFAQHGCKVIIADIDDKNGLSVAEEIGPEYALFIHCD
                              VTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC
                                                                                             129 MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN
                                                                                                                                                              CLSPFGLPTALGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDEAKYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
NCBI_TaxID=3654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ing or three gibberellin-regulated cDNAs from watermelon during seed development; down-regulated one cDNA and up-regulated two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
6
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Kim J., Kang H., Jun S., Lee J., An G.;
"Cloning of three gibberellin-regulated cDNAs from watermelon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 AA; 28835 MW; 904A835DDD52B6E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Citrullus lanatus (Watermelon) (Citrullus vulgaris).
                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.8%; Score 665.5; DB 10
51.1%; Pred. No. 1.7e-42;
tive 48; Mismatches 74
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                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                 (SDR) FAMILY.
EMBL; AB018559; BAA89230.1;
HSSP; P19992; 1HDC.
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Matches 137; Conservative
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01-MAY-2000 (
01-MAY-2000 (
01-DEC-2001 (
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                                                                                                                                         VINEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
                                                                                                                                                                                                           MKHAARVMIPARSGNIISTASLSSTMGGGSSHAYCGSKHAVLALTRNLAVELGQFGIRVN 188
                                                                                                                                                                                                                            CLSPFGLPTALGKKFSGIKNEEFFENVINFAGNLKGPKFNVEDVANAALYLASDEAKYVS 248
                                                                                                                                                                        VRIESHVQHAVDTTVSRYGKLDIMFSNAGVAGSRDTSILEASPENINLVFETNVFGAFFC 131
                                                                                                                                                                                                                                                                                               KRLEGKVAIITGAANGIGATTARLFAQHGCKVIIADIDDKNGHSVAEEIGPEYALFIHCD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
                                                                          9 RRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAIGTSNSTYIHCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H77-2;
Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Kowyama Y.;
Tsuchiya T., Suwabe K., Watase T., Kagaya Y., Kowyama Y.;
"Characterization of promoter region of the SSP gene from Ipomoea
trifida regulates stigma-specific expression.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kowyama Y., Kadotta N., Sassa H., Kakeda K., Tsuchiya T., Ishimizu T Kondo K., Norioka S., Salotus specific stigma protein (SSP) from sporophytic self-incompatibility plant, Ipomoea trifida, is a member of short-chain alcohol dehydrogenase family."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ipomoea trifida.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Convolvulaceae, Ipomoea.
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                                             84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Short-chain alcohol dehydrogenase (S-locus linked stigma
               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       277 AA; 29257 MW; A0CDB434B31C666D CRC64;
           Score 670; DB 10;
Pred. No. 8.1e-43;
41; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                         277 AA
                                                                                                                                                                                                                                                                                                                                         GHNLFIDGGFSVCNSVIKV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002198; ADH short.
Pfam; PF00106; adh short; 1.
PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF072449; AAC35342.1; -. EMBL; AB070221; BAB86916.1; -.
                                                                                                                                                                                                                                                                                                                                                                        GLNLLIDGGFTTTNIAFOV
             48.1%;
                                             Conservative
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SEQUENCE FROM N.A.

CASTRAINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

MEDLINE-21016719; PubMed=11130712;

MA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Manite C., Alonso J., Altafi H., Araujo R.P., Chon C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

M. Gill J.E., Goldsmith A.D., Hanse B., Hansen N.F., Hughes B., Huizar L.,

M. Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

K. K., Koo H.L., Kremnetekaia I., Kurtz D.B., Kwan A., Lam B.,

M. Langin-Hooper S., Lee A., Leer C.A., Lid J.H., Li Y.-P.,

M. Lin X., Liu S.X., Liu Z.A., Luros J.S., Matti R., Marziali A.,

M. Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Tallon L.J., Tambunga G., Tortiumi M.J., Town C.D.,

Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

M. D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Nathian A. M. Saquence and analysis of chromosome I of the plant Arabidopsis
                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Short chain alcohol dehydrogenase, putative (Short-chain dehydrogenase/reductase).
F19K6.3 OR ABA2 OR ATIG52340.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sprartophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Streptosia II; Brassicales; Brassicacee; Arabidopsis.
NCBL_TaxID=3702;
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Bah J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narraska M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.,

Submitted (Apr. 2002) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES

(SDR) FAMILY.
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Cheng W.-H., Endo A., Zhou L., Penney J., Chen H.-C., Arroyo A.,
Leon P., Nambara E., Asami T., Seo M., Koshiba T., Sheen J.;
Lan P., Nambara E., Asami T., Seo M., Koshiba T., Sheen J.;
La unique short-chain dehydrogenase/reductase in Arabidopsis glucose
signaling and abscrisic acid biosynthesis and functions.";
Submitted (MAR-2002) to the EMBL/Genbank/pDBJ databases."
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BMBL, AY082244; AAL92237.1; --
EMBL, AY082045; AAL92237.1; --
EMBL, AY095603; AAM20454.1; --
HSSP, P29123; LDFI
INTERPTO; IPR002198; ADH_short.
INTERPTO; IPR002198; ADH_short.
PRINTS; PR00106; add_short; 1.
PRINTS; PR001061; ADH_SHORT; 1.
Oxidoreductase.
SEQUENCE 285 AA; 30272 MM; 8B
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133 AKHAARVMIPAKKGSIVFTASISSFTAGEGVSHVYTATKHAVLGLTTSLCTELGEYGIRV 192
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ARRLEGKVALITGGASGIGETTAKLFSQHGAKVAIADVQDELGHSVVEAI--GTSNST--
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Xia Z.Q., Costa M.A., Pellssier H.C., Davin L.B., Lewis N.G.;
Xia Z.Q., Costa M.A., Pellssier H.C., Davin L.B., Lewis N.G.;
Xia Z.Q., Costa M.A., Pellssier H.C., Davin L.B., Lewis N.G.;
Secoisolaricizesinol Debydrogenase Purification, Cloning, and
Functional Expression. IMPLICATIONS FOR HUMAN HEALTH PROTECTION.";
J. Biol. Chem. 276:12614-12623(2001)
J. Biol. Chem. 276:12614-12623(2001)
J. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
EMBL, APIS27734; AAX38664.1;
InterPro; IPR0020298; ADL short.
InterPro; IPR0010598; ADL short.
InterPro; IPR00106; adh short;
IPROSITE; PR00106; adh short;
PROSITE; PR00106; ADL SHORT;
IPROSITE; PR00106; 
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01-DEC.2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Philizome secoisolariciresinol dehydrogenase (Fragment).
Podophyllum peltatum (Mayapple).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Berberidaceae; Magnollophyta; eudicotyledons; Ranunculales;
111 TaxID-35933;
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46.8%; Score 652.5; DB 10; Length 278;
Best Local Similarity 52.2%; Pred. No. 1.7e-41;
Matches 133; Conservative 43; Mismatches 76; Indels 3;
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NON_TER 278 A4, 29253 MW; DB735A376E112375 CRC64;
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                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thallana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 44.9%; Score 625.5; DB 10; Length 303; Local Similarity 47.5%; Pred. No. 2e-39; Nes 131; Conservative 52; Mismatches 78; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deleeny M., Berger C., Cooke R., Grellet F., Laudie M., Mewes
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.,
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 AA; 32151 MW; DC1BD28DABE38DD6 CRC64;
                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Short-chain alcohol dehydrogenase-like protein.
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                      T18N14.60.
Arabidopsis thaliana (Mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AL132968; CAB63154.1; -.. HSSP; P19992; 1HDC. InterPro; PR002198; ADH short. Ffam; PF00106; adh short; 1.. PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH_SHORT; 1.
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01-MAY-1999 (TrEMBLrel. 10, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Putative alcohol dehydrogense.
                                           SGLNLVIDGGYTRIN 266
                SCHNLFIDGGFSVCN
                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
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                248
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Q9ZR17
ID Q9ZR1
AC Q9ZR1
DT 01-MA
DT 01-MA
DF 01-MA
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09SCU0
AC 09SCU0
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69 VTNEDGVKNAVDNTVSTYGKLDIMFSNAGISDPNRPRIIDNEKADFERVLSVNVTGVFLC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLSPFGLPTA-----LGKKFSGIKNEEEFENVINFAGNLKGPKFNVEDVANAALYLASDE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K., Mayer K.F.X., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                "Arabidopsis thaliana BAC F4C21 from chromosome IV near 17 cM."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                Habermann K., de la Bastide M., Huang E.N., Gnoj L., Schutz K.
Preston R., Calma C., Martienssen R., Parnell L.D., Dedhia N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AA; 29994 MW; 93B0A97CECC859BC CRC64;
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42.9%; Score 597.5;
Best Local Similarity 47.0%; Pred. No. 2.4e
Matches 126; Conservative 45; Mismatches
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EMBL; AL161496; CAB77799.1; -.
HSSP; P19922; 1HDC.
InterPro; IPR002198; ADH_short.
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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McCombie W.R.;
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